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OM protein - protein search, using sw model

Run on: May 12, 2003, 08:48:58 ; Search time 13.7288 Seconds
(without alignments)
771.534 Million cell updates/sec

Title: US-09-980-881A-2

Perfect score: 1911

Sequence: 1 MKLSLAVLPVILFCEQHV.....IKSFTSNPYEKLLPLSLK 360

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents-AA: *
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/Backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1817	95.1	386	4	US-09-813-133A-2
2	1799.5	94.2	423	1	US-07-649-591B-3
3	1799.5	94.2	423	1	US-08-277-540-3
4	1799.5	94.2	423	1	US-08-430-787A-3
5	1799.5	94.2	423	2	US-08-869-057-2
6	1788.5	93.5	423	4	US-09-813-133A-4
7	640.5	33.5	404	1	US-08-696-138-2
8	639	33.4	415	2	US-08-860-882A-57
9	639	33.4	415	4	US-09-011-769A-39
10	631.5	33.0	424	4	US-09-011-769A-56
11	628.5	32.9	417	1	US-07-649-591B-7
12	628.5	32.9	417	1	US-08-277-540-7
13	628.5	32.9	417	1	US-08-430-787A-7
14	623	32.6	716	4	US-09-171-945-125
15	619.5	32.4	417	1	US-07-649-591B-6
16	619.5	32.4	417	1	US-08-277-540-6
17	619.5	32.4	417	1	US-08-430-787A-6
18	604	31.6	307	2	US-08-782-760-6
19	604	31.6	307	2	PCF-US96-00995-6
20	604	31.6	437	4	US-09-675-305-10
21	603.5	31.6	396	1	US-07-649-591B-4
22	603.5	31.6	396	1	US-08-277-540-4
23	603.5	31.6	396	1	US-08-430-787A-4
24	576	30.1	306	1	US-08-696-138-4
25	561	29.4	329	4	US-09-011-769A-51
26	561	29.4	349	4	US-09-011-769A-47
27	554	29.0	349	4	US-09-011-769A-60

28	553	28.9	349	4	US-09-011-769A-64	Sequence 64, Appl
29	553	28.9	417	1	US-07-649-591B-8	Sequence 8, Appl
30	553	28.9	417	1	US-08-277-540-8	Sequence 8, Appl
31	553	28.9	417	1	US-08-430-787A-8	Sequence 8, Appl
32	546	28.6	399	4	US-09-171-945-113	Sequence 113, App
33	543	28.4	613	4	US-09-675-305-12	Sequence 12, Appl
34	528.5	27.7	350	4	US-07-649-591B-5	Sequence 5, Appl
35	528.5	27.7	419	1	US-08-277-540-5	Sequence 5, Appl
36	528.5	27.7	419	1	US-08-430-787A-5	Sequence 5, Appl
37	528.5	27.7	419	1	US-09-171-945-113	Sequence 6, Appl
38	519.5	27.2	436	4	US-09-675-305-10	Sequence 4, Appl
39	513	26.8	417	4	US-08-640-906-4	Sequence 4, Appl
40	513	26.8	417	4	US-09-395-936-4	Sequence 18, Appl
41	512	26.8	417	4	US-08-640-906-18	Sequence 18, Appl
42	512	26.8	417	4	US-08-395-936-18	Sequence 2, Appl
43	487.5	25.5	419	4	US-08-640-906-2	Sequence 2, Appl
44	487.5	25.5	419	4	US-09-395-936-2	Sequence 2, Appl
45	482.5	25.2	419	4	US-08-640-906-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-2
Sequence 2, Application US/09813133A
Patent No. 6455294
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
FILE REFERENCE: C1001173
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 386
TYPE: PRT
ORGANISM: Human
US-09-813-133A-2

Query Match 95.1%; Score 1817; DB 4; Length 386;

Best Local Similarity 98.6%; Pred. No. 8.2e-189;

Matches 341; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY	1	MKLSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQOVONLTTTYEIVLMQPTAD	60
DB	1	MKLSLAVLPVILFCEQHVAFQSGQVLAALPRTSRQOVONLTTTYEIVLMQPTAD	60
QY	61	LIYKKQVHFVNASDVNKAHLNVSIGTFCVLAADVELLIDQOISNDVSPRASASY	120
DB	61	LIYKKQVHFVNASDVNKAHLNVSIGTFCVLAADVELLIDQOISNDVSPRASASY	120
QY	121	EQYHSLNEIYTWIEFTTERPDMLTKIHGSSFEKPLYLAKSGEQRKNAIWDGCI	180
DB	121	EQYHSLNEIYTWIEFTTERPDMLTKIHGSSFEKPLYLAKSGEQRKNAIWDGCI	180
QY	181	HAREWISPAFCWFIHGNRMRRNRSFYANNHCIGTDLNSFVSKHWCCEGASSCSET	240
DB	181	HAREWISPAFCWFIHGNRMRRNRSFYANNHCIGTDLNSFVSKHWCCEGASSCSET	240
QY	241	YCGLYPSEPEVAAVSFLRRNINQIKAYISMSYSQHIYFPYSYRSKSKDHEELSLVA	300
DB	241	YCGLYPSEPEVAAVSFLRRNINQIKAYISMSYSQHIYFPYSYRSKSKDHEELSLVA	300
QY	301	SEAVRAIDKTSKNTRYTHGSETLYLAPGGDDWIYDLGIKYSFT	346
DB	301	SEAVRAIDKTSKNTRYTHGSETLYLAPGGDDWIYDLGIKYSFT	346

US-07-649-591B-3
Sequence 3, Application US/07649591B
Patent No. 5206161
GENERAL INFORMATION:
APPLICANT: Dennis Drayna and Daniel Eaton
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649,591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-3

Query Match 94.2%; Score 1799.5; DB 1; Length 423;
Best Local Similarity 89.6%; Pred. No. 7.6e-187;
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;

QY 1 MKLCSLAVLPVPLVPCQHVFAFGSGGYLAALPRTSROYVQLONTTYYEIVLMQPVAD 60
DB 1 MKLCSLAVLPVPLVPCQHVFAFGSGGYLAALPRTSROYVQLONTTYYEIVLMQPVAD 60
QY 61 LTVKKQVHFEVNASDVNVKAKHLNVSIGPCSVLLADVEDLIQOQISNDTVSPRASASY 120
DB 61 LTVKKQVHFEVNASDVNVKAKHLNVSIGPCSVLLADVEDLIQOQISNDTVSPRASASY 120
QY 121 EGYHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEXKPLYVLKVSKEQTAKNAIWDGCI 180
DB 121 EGYHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEXKPLYVLKVSKEQTAKNAIWDGCI 180
QY 181 HAREMISPAFCMLFTIGH-----NRMWRK 203
DB 181 HAREMISPAFCMLFTIGH-----NRMWRK 203
QY 204 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 263
DB 204 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 263
QY 241 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 300
DB 241 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 300
QY 324 TLYLAPGGDDMIYDLGKIYSFT 346
DB 324 TLYLAPGGDDMIYDLGKIYSFT 346
QY 361 TLYLAPGGDDMIYDLGKIYSFT 383
DB 361 TLYLAPGGDDMIYDLGKIYSFT 383

RESULT 3
US-08-277-540-3
Sequence 3, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-3

Query Match 94.2%; Score 1799.5; DB 1; Length 423;
Best Local Similarity 89.6%; Pred. No. 7.6e-187;
Matches 343; Conservative 1; Mismatches 2; Indels 37; Gaps 1;

QY 1 MKLCSLAVLPVPLVPCQHVFAFGSGGYLAALPRTSROYVQLONTTYYEIVLMQPVAD 60
DB 1 MKLCSLAVLPVPLVPCQHVFAFGSGGYLAALPRTSROYVQLONTTYYEIVLMQPVAD 60
QY 61 LTVKKQVHFEVNASDVNVKAKHLNVSIGPCSVLLADVEDLIQOQISNDTVSPRASASY 120
DB 61 LTVKKQVHFEVNASDVNVKAKHLNVSIGPCSVLLADVEDLIQOQISNDTVSPRASASY 120
QY 121 EGYHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEXKPLYVLKVSKEQTAKNAIWDGCI 180
DB 121 EGYHSLNEIYSWIEFTTERHPDMLTKIHIGSSFEXKPLYVLKVSKEQTAKNAIWDGCI 180
QY 181 HAREMISPAFCMLFTIGH-----NRMWRK 203
DB 181 HAREMISPAFCMLFTIGH-----NRMWRK 203
QY 204 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 263
DB 204 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 263
QY 241 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 300
DB 241 NNSFYANNHCIGTDLNRSNFVSKHMCCEGASSSCSETYCGLYPESPEPVKAVASFLRNI 300

TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-7

Query Match 32.9%; Score 628.5; DB 1; Length 417;
Best Local Similarity 37.0%; Pred. No. 1.3e-59;
Matches 140; Conservative 60; Mismatches 131; Indels 47; Gaps 8;

QY 6 LAVLVPIVLFCEQHVAFOSGOVLALPRTSRQOVOLNLTTEYELVLMQPTADLIYVK 65
DB 7 MAVIYTTLALAPVH---FDEKVFERYKLVONEKHAASVYKNTLSIEDFWPDAIHDIYAVN 63
QY 66 KOVHFVNASDVNDVNAKHLNVSGIPCSVLLADVEDLIQOQIS-NDTVSPRASASYEYOH 124
DB 64 MYDFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDELACHRS---YAKYN 120
QY 125 SLNEIYSWIEFTEIRHPDMLTKIHIGSSFEKPYLYLVKSGKQOTAKNAIMWDCGIHARE 184
DB 121 DMWKIVSWTEKMLEKHPEWVSRIKISTVEDNPLYVYKTI-GKKDGERKAIFFMDCGIHARE 179
QY 185 WISPAFLCMEFI-----GHN-----RMRKRRRSF 207
DB 180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFYLPVFNVDGYIMSWQDRMRKRRSR 239
QY 208 YANNHCIGTDLNSNFVSKHWCCEGASSSCSEFYCGLYPESEPEVKAVASFLRRNINQIK 267
DB 240 NONSTCIGDNLNMF-DVSDMSSPNTNKPCLNRYRGPAPSEKETAVNTFIRSHINSIK 298
QY 268 AYISMHSYQHIYFEPYSYTRSKSKDHEELSLVASEAVRAIDKTSKTRTYTHGSETLYL 327
DB 299 AYITFHSYSQMLLIPYGYTFKLPNNHODLKVARIATDAL-STREYFRYIYGPDIASYIK 357
QY 328 APGGDDMIYDLGIKYSF 345
DB 358 TSGSSLDWYVDLGIKHTF 375

RESULT 12
US-08-277-540-7
Sequence 7, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277, 540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-7

Query Match 32.9%; Score 628.5; DB 1; Length 417;
Best Local Similarity 37.0%; Pred. No. 1.3e-59;
Matches 140; Conservative 60; Mismatches 131; Indels 47; Gaps 8;

QY 6 LAVLVPIVLFCEQHVAFOSGOVLALPRTSRQOVOLNLTTEYELVLMQPTADLIYVK 65
DB 7 MAVIYTTLALAPVH---FDEKVFERYKLVONEKHAASVYKNTLSIEDFWPDAIHDIYAVN 63
QY 66 KOVHFVNASDVNDVNAKHLNVSGIPCSVLLADVEDLIQOQIS-NDTVSPRASASYEYOH 124
DB 64 MYDFRVSEKESQTIQSTLEQHKIHYEILIHDLQEEIEKQFDVKDELACHRS---YAKYN 120
QY 125 SLNEIYSWIEFTEIRHPDMLTKIHIGSSFEKPYLYLVKSGKQOTAKNAIMWDCGIHARE 184
DB 121 DMWKIVSWTEKMLEKHPEWVSRIKISTVEDNPLYVYKTI-GKKDGERKAIFFMDCGIHARE 179
QY 185 WISPAFLCMEFI-----GHN-----RMRKRRRSF 207
DB 180 WISPAFCQWFVYQATKSYGKNKIMTKLLDRMNFYLPVFNVDGYIMSWQDRMRKRRSR 239
QY 208 YANNHCIGTDLNSNFVSKHWCCEGASSSCSEFYCGLYPESEPEVKAVASFLRRNINQIK 267
DB 240 NONSTCIGDNLNMF-DVSDMSSPNTNKPCLNRYRGPAPSEKETAVNTFIRSHINSIK 298
QY 268 AYISMHSYQHIYFEPYSYTRSKSKDHEELSLVASEAVRAIDKTSKTRTYTHGSETLYL 327
DB 299 AYITFHSYSQMLLIPYGYTFKLPNNHODLKVARIATDAL-STREYFRYIYGPDIASYIK 357
QY 328 APGGDDMIYDLGIKYSF 345
DB 358 TSGSSLDWYVDLGIKHTF 375

RESULT 13
US-08-430-787A-7
Sequence 7, Application US/08430787A
Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430, 787A
FILING DATE: 27-APR-1995

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US-07-649-591B-3
Sequence 3, Application US/07649591B
Patent No. 5206161
GENERAL INFORMATION:
APPLICANT: Dennis Drayna and Daniel Eaton
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649,591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-3

Query Match 94.5%; Score 1699.5; DB 1; Length 423;
Best Local Similarity 89.8%; Pred. No. 1e-174; Indels 37; Gaps 1;
Matches 324; Conservative 0; Mismatches 0;

QY 1 FOSGOVLALPRTSRQVOVLONTTTEYELVLMQPTADLIVKKKQVHFVNASDVNVKA 60
DB 23 FOSGOVLALPRTSRQVOVLONTTTEYELVLMQPTADLIVKKKQVHFVNASDVNVKA 82

QY 61 HLNVSIGPISVLLADVEDLIQOQISNDTVSPRASASYEYHSLNETYSWIEFITERHPD 120
DB 83 HLNVSIGPISVLLADVEDLIQOQISNDTVSPRASASYEYHSLNETYSWIEFITERHPD 142

QY 121 MLTKIHGSSFEKYPYLVKVSKEQOTAKNAIWDGCHAREWISPAFLMFIQHTQFY 175
DB 143 MLTKIHGSSFEKYPYLVKVSKEQOTAKNAIWDGCHAREWISPAFLMFIQHTQFY 202

QY 176 -----NRMWRKRSFYANNHCIGTDLNRNFASK 203
DB 203 GIIGQYTNLLRLVDYVMPVNVNDGYDSWKKNRMKRSFYANNHCIGTDLNRNFASK 262

QY 204 HMCCEGASSSCSEYTCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSGHIYFPYSY 263
DB 263 HMCCEGASSSCSEYTCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSGHIYFPYSY 322

QY 264 TRKSDHEELSLVASEAVNAIETKSNRPTHGSESTLYLAPGGDDMIVDLGIKYSF 323
DB 323 TRKSDHEELSLVASEAVNAIETKSNRPTHGSESTLYLAPGGDDMIVDLGIKYSF 382

QY 324 T 324
DB 383 T 383

RESULT 3
US-08-277-540-3
Sequence 3, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: palin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-3

Query Match 94.5%; Score 1699.5; DB 1; Length 423;
Best Local Similarity 89.8%; Pred. No. 1e-174; Indels 37; Gaps 1;
Matches 324; Conservative 0; Mismatches 0;

QY 1 FOSGOVLALPRTSRQVOVLONTTTEYELVLMQPTADLIVKKKQVHFVNASDVNVKA 60
DB 23 FOSGOVLALPRTSRQVOVLONTTTEYELVLMQPTADLIVKKKQVHFVNASDVNVKA 82

QY 61 HLNVSIGPISVLLADVEDLIQOQISNDTVSPRASASYEYHSLNETYSWIEFITERHPD 120
DB 83 HLNVSIGPISVLLADVEDLIQOQISNDTVSPRASASYEYHSLNETYSWIEFITERHPD 142

QY 121 MLTKIHGSSFEKYPYLVKVSKEQOTAKNAIWDGCHAREWISPAFLMFIQHTQFY 175
DB 143 MLTKIHGSSFEKYPYLVKVSKEQOTAKNAIWDGCHAREWISPAFLMFIQHTQFY 202

QY 176 -----NRMWRKRSFYANNHCIGTDLNRNFASK 203
DB 203 GIIGQYTNLLRLVDYVMPVNVNDGYDSWKKNRMKRSFYANNHCIGTDLNRNFASK 262

QY 204 HMCCEGASSSCSEYTCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSGHIYFPYSY 263
DB 263 HMCCEGASSSCSEYTCGLYPESEPEVKAVASFLRRNINQIKAYISMHSYSGHIYFPYSY 322

OY	264	TRRSKQHEELSLVASEAVRAIEKTSKNRTYRTHGSEETLYLAPGGDDMDIYDLGIKYSF	323
Db	323	TRRSKQHEELSLVASEAVRAIEKTSKNRTYRTHGSEETLYLAPGGDDMDIYDLGIKYSF	382
OY	324	T	324
Db	383	T	383

RESULT 4

US-08-430-787A-3
Sequence 3, Application us/08430787A
Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Dayana, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5593674e1 Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,787A
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,540
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28, 616
REFERENCE/DOCKET NUMBER: 68BD1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-430-787A-3

Query Match	94.5%;	Score 1639.5;	DB 1;	Length 423;
Best Local Similarity	89.8%;	Pred. No. 1e-174;	0;	Indels 37;
Matches 324;	Conservative	0;	Mismatches	Gaps 1

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QY 1 FOSQOVLALPRTSROYVLONLTTTTEIYLMOPVTADLLVKKKOVHFNFNASDVONVA 60
Db 23 FOSQOVLALPRTSROYVLONLTTTTEIYLMOPVTADLLVKKKOVHFNFNASDVONVA 82
QY 61 HLANSGIPC SVLLADVEDLIQQQISNDTVSPRASASYEYQHSINLETNYSWIEFTERRHPD 120
Db 83 HLANSGIPC SVLLADVEDLIQQQISNDTVSPRASASYEYQHSINLETNYSWIEFTERRHPD 142
QY 121 MLTNIHGSSEKRPVLYKVSCEQJAKANLWDCSIHAREWISPAFLCMPTIGH----- 175

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Db      143  MLTRIHIGSSPEKPEVLVLYKXSGKEQYAKNAIWIIDCGIHAHEWISPAFLCMIFGHIQFY 202
QY      176  -----NMKRNKNSFYANNHCIGTDLNRNPAK 203
Db      203  GIIQYTNLRLVDFYVWPVYVNVGDYDYSWKNNMWRKNSFYANNHCIGTDLNRNPAK 262
QY      204  HMCEGASSSCSEFTYVGLYPESEPEYKAAVAFLLRNINQIKATISMHSYQHTVPFYSY 263
Db      263  HMCEGASSSCSEFTYVGLYPESEPEYKAAVAFLLRNINQIKATISMHSYQHTVPFYSY 322
QY      264  TRRSKSDHEELSLVAEAVRAIEKTSKNTRYTHGSETLYLAFGGDDWIYDLGIRYSF 323
Db      323  TRRSKSDHEELSLVAEAVRAIEKTSKNTRYTHGSETLYLAFGGDDWIYDLGIRYSF 382
QY      324  T 324
Db      383  T 383

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RESULT

```

US-08-869-057-2
Sequence 2, Application US/08869057
Patent No. 5985562
GENERAL INFORMATION:
APPLICANT: Morser, Michael J
APPLICANT: Nagashima, Mariko
TITLE OF INVENTION: Method of Detecting Thrombotic Disease
TITLE OF INVENTION: Risk
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Berlex Biosciences Legal Department
STREET: 15049 San Pablo Avenue
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804-0099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,057
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Washlien, Wendy L
REGISTRATION NUMBER: 36,301
REFERENCE/DOCKET NUMBER: 51509AUSM1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-262-5411
TELEFAX: 510-262-7095
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
TISSUE TYPE: Plasma
FEATURE:
NAME/KEY: Peptide
LOCATION: 23..401
US-08-869-057-2

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Query Match	94.5%	Score	1699.5	DB	2	Length	423
Best Local Similarity	89.8%	Pred. No.	1e-174				
Matches	324	Conservative	0	Mismatches	0	Indels	37
						Gaps	1

Qy 1 FOSGCVLALPRTSRQVVLQNLTITYEIVMQPVADLVKKQHFFVNASDVNVKA 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 23 FQSGCVLALPRTSRQVVLQNLTITYEIVLMQPVADLVKKQHFFVNASDVNVKA 82


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Db      80 VLKNELOAYKVILSNLRNVVDAQEDSRV---RATGSHSEYXKNMKWETLEAWTOQVATENPA 136
Oy     121 MLTNIHIGSSSEKEPLVYLAKNSGGEQJAKNNAIMIDCGIHAREMISPAFLMTI----- 173
       :::: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db     137 LISRSVIOTTEGRALYLLKV-GRAGONKRAPIFMDCGFHAEWISPAFCOMFEAREVRTY 195
Oy     174 -----GH-----NEMWRKRNSFEYANNHCIGTDLNRNFASK 203
       |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db     196 GREIOVELLDKLPFYVLPLYUNIDIGITYITWTKSFRPKRTKSTHTGGSSCIGTDPRKRF-DA 254
Oy     204 HMCEGASSSSCSETGYCYGLYPESEPEYKAVASPLRRINIQIKAYISMHSYQHILVPFSY 263
       |||| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db     255 GWCELGASRNPCDETYCGPAAESKEKETRALADFI RNKLSSIKAVLTTHSYSQMMIYYYSY 314
Oy     264 TRSKSKDHEELSVASEVAIRIEKTSKNTRTTHGSETTLAPAGGDDMYIDLGIYSF 322
       :::: |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db     315 AYKLGENNALMALAKATVKEL-ASHLQTKYTYPGATITTPAAGSGSDWAYDOGIRYSF 373
Oy     324 T 324
       |
Db     374 T 374

RESULT 9
US-09-011-769A-39
Sequence 39, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
          BLAKEY, David C.
          DAVIES, David H.
          HENNAM, John F.
          HENNEQUIN, Laurent F.A.
          MARSHAM, Peter R.
          DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011.769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39
Query Match           35.5%; Score 637.5; DB 4; Length 415;
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-7

Query Match
Best Local Similarity 35.2%; Score 632; DB 1; Length 417;
Matches 138; Conservative 57; Mismatches 122; Indels 44; Gaps 7;

1 FOSGOVLALPRTSROYVQLNTTVEIYLMOPVTADLIYKKQVHEFNASDVNDVKA 60
21 FDRKVEYRVKLQNEKHAVALKNTQSLDEFWPDALHDAVNMVDFRVSEKESQTIOS 80
61 HUNVSGIPCSVLADVEDLIQOQIS-NDTVSPRASASYEQYHSLSNFIYSWIEFITERHP 119
81 TLEQHKIHEILLHDLOEIEKQFDVKDELTAGRHS--YAKYNDWDKIVSWTEKMLEKHP 137
120 DMLTKHIGSFEPKPYLYLVKSGKEOTAKNAIMIDCGIHAREWISPAFCMLMT----- 173
138 EMWSRIKIGSTVEDNPLYLKI-GKKDGERKALFMDCGIHAREWISPAFCOMFYQATKS 196
174 -GHN-----RMKRNRSFYANNHCIGTDLNRNFA 202
197 YGKNKIMTKLDRMNFYVLPFVNDGYIMSWTODRMKRNRSNOSTCIGTDLNRNF-D 255
203 KHWCEGASSSSCSEYTCGLYPESEPEVKAASFRRNIQIKAYISMHSYQHIYVPS 262
256 VSMDSPTNTKPCLVNVRGPAPESEKETKAVTNFIRSHLSIKAYIFHYSQMLLPYG 315
263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHSEFTLYLAPGGDDWIDLGIKYS 322
316 YTRKLPNHODLKVARIADAL-STRETRYIYGPILASTIYKTSGLDWDVLDGIKHT 374

323 F 323
375 F 375

RESULT 12
US-08-277-540-7
Sequence 7, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-7

Query Match
Best Local Similarity 35.2%; Score 632; DB 1; Length 417;
Matches 138; Conservative 57; Mismatches 122; Indels 44; Gaps 7;

1 FOSGOVLALPRTSROYVQLNTTVEIYLMOPVTADLIYKKQVHEFNASDVNDVKA 60
21 FDRKVEYRVKLQNEKHAVALKNTQSLDEFWPDALHDAVNMVDFRVSEKESQTIOS 80
61 HUNVSGIPCSVLADVEDLIQOQIS-NDTVSPRASASYEQYHSLSNFIYSWIEFITERHP 119
81 TLEQHKIHEILLHDLOEIEKQFDVKDELTAGRHS--YAKYNDWDKIVSWTEKMLEKHP 137
120 DMLTKHIGSFEPKPYLYLVKSGKEOTAKNAIMIDCGIHAREWISPAFCMLMT----- 173
138 EMWSRIKIGSTVEDNPLYLKI-GKKDGERKALFMDCGIHAREWISPAFCOMFYQATKS 196
174 -GHN-----RMKRNRSFYANNHCIGTDLNRNFA 202
197 YGKNKIMTKLDRMNFYVLPFVNDGYIMSWTODRMKRNRSNOSTCIGTDLNRNF-D 255
203 KHWCEGASSSSCSEYTCGLYPESEPEVKAASFRRNIQIKAYISMHSYQHIYVPS 262
256 VSMDSPTNTKPCLVNVRGPAPESEKETKAVTNFIRSHLSIKAYIFHYSQMLLPYG 315
263 YTRSKSKDHEELSLVASEAVRAIEKTSKNTRYTHGHSEFTLYLAPGGDDWIDLGIKYS 322
316 YTRKLPNHODLKVARIADAL-STRETRYIYGPILASTIYKTSGLDWDVLDGIKHT 374

323 F 323
375 F 375

RESULT 13
US-08-430-787A-7
Sequence 7, Application US/08430787A
Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,787A
FILING DATE: 27-APR-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,540
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-430-787A-7

Query Match 35.2%; Score 632; DB 1; Length 417;
Best Local Similarity 38.2%; Pred. No. 1.4e-59;
Matches 136; Conservative 57; Mismatches 122; Indels 44; Gaps 7;

QY 1 FOSQVLAALPRTSROYVLONTTTEIYVLMQPTADLIYKKQVHFVNASDVNVKA 60
DB 21 FDRKVFVRVVKQNKHSAVYKLNLOSTELDFWDALHIDVNNVTDFRVSSEKSOIIO 80
QY 61 HLVNSGIPCSVLADVEDLLOOQIS-NDTVSPRASASYEOYHSLNEIYSIEFITERHP 119
DB 81 TLEQKHITHELLHIDLOEIEKQFDVDELAGRHS---YAKYNDMDIVSWTEMLKHP 137
QY 120 DMLTKIHGSEFEKPYLVKVSKEQOTAKNAIWDGCIHAREMISPAFCWMT----- 173
DB 138 EMVSRKIGTSTVEDNPLYVKI-GRKQERKALFMDGCIHAREMISPAFCWMT----- 196
QY 174 -GHN-----RMWRKRSFYANNHCIGTDLNRNFS 202
DB 197 YGRNKIMTKLLDRMNFYILPVFNVDGYIWSWTQDRMRKNSRNSQSTCIGTDLNRNF-D 255
QY 203 KHNCEGASSSCSEETCYGLYPESEPEVKAVASFLRRNINOIKAYISMHSQHIYFYS 262
DB 256 VSMDSSTNTKPCPLNVYRGAPPESEKETKAVTNFIRSHLSIKAVITFHSYSQMLLPYG 315
QY 263 YTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGSEETLYLAPGGDDMIYDLGIKYS 322
DB 316 YTRKLPNHDLLKVAIAIADAL-STREYTRYIYGPILASTIYKTSGLSDWVYDLGIKHT 374
QY 323 F 323
DB 375 F 375

RESULT 14
US-07-649-591B-6
Sequence 6, Application US/07649591B
Patent No. 5206161
GENERAL INFORMATION:
APPLICANT: Dennis Drayna and Daniel Eaton
TITLE OF INVENTION: NO. 5206161el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California

COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649,591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 417 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-6

Query Match 34.6%; Score 622; DB 1; Length 417;
Best Local Similarity 35.5%; Pred. No. 1.7e-58;
Matches 128; Conservative 71; Mismatches 118; Indels 44; Gaps 7;

QY 1 FOSQVLAALPRTSROYVLONTTTEIYVLMQPTADLIYKKQVHFVNASDVNVKA 60
DB 21 FDRKVFVRVVKQNKHSAVYKLNLOSTELDFWDALHIDVNNVTDFRVSSEKSOIIO 80
QY 61 HLVNSGIPCSVLADVEDLLOOQIS-NDTVSPRASASYEOYHSLNEIYSIEFITERHP 119
DB 81 ALDQNKHITHELLHIDLOEIEKQFDVDEIPIGRHS---YAKYNDMDIVSWTEMLKHP 137
QY 120 DMLTKIHGSEFEKPYLVKVSKEQOTAKNAIWDGCIHAREMISPAFCWMT----- 173
DB 138 EMVSRKIGTSTVEDNPLYVKI-GRKQERKALFMDGCIHAREMISPAFCWMT----- 196
QY 174 -GHN-----RMWRKRSFYANNHCIGTDLNRNFS 202
DB 197 YGRNKIMTKLLDRMNFYILPVFNVDGYIWSWTQDRMRKNSRNSQSTCIGTDLNRNF-N 255
QY 203 KHNCEGASSSCSEETCYGLYPESEPEVKAVASFLRRNINOIKAYISMHSQHIYFYS 262
DB 256 ASMNSIINTDPCADNIRGAPPESEKETKAVTNFIRSHLSIKAVITFHSYSQMLLPYG 315
QY 263 YTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGSEETLYLAPGGDDMIYDLGIKYS 322
DB 316 YTRKLPNHDLLKVAIAIADAL-STREYTRYIYGPILASTIYKTSGLSDWVYDLGIKHT 374
QY 323 F 323
DB 375 F 375

RESULT 15
US-08-277-540-6
Sequence 6, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: NO. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

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GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 12, 2003, 08:48:58 ; Search time 9.38136 Seconds
(Without alignments)
771.534 Million cell updates/sec

Title: US-09-980-881a-4

Perfect score: 1338

Sequence: 1 ASASYEQYHSLNIEYSMIE.....IKYFTSNPVEKILPLSLK 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/plodata/1/1aa/5A.COMB.pep.*
3: /cgn2_6/plodata/1/1aa/5B.COMB.pep.*
4: /cgn2_6/plodata/1/1aa/6A.COMB.pep.*
5: /cgn2_6/plodata/1/1aa/6B.COMB.pep.*
6: /cgn2_6/plodata/1/1aa/6C.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1257	93.9	386	US-09-813-133A-2	Sequence 2, Appli
2	1239.5	92.6	423	US-07-649-591B-3	Sequence 3, Appli
3	1239.5	92.6	423	US-08-277-540-3	Sequence 3, Appli
4	1239.5	92.6	423	US-08-430-787A-3	Sequence 3, Appli
5	1239.5	92.6	423	US-08-869-057-2	Sequence 2, Appli
6	1228.5	91.8	423	US-09-813-133A-4	Sequence 4, Appli
7	610	45.6	307	US-08-782-760-6	Sequence 6, Appli
8	610	45.6	307	PCT-US96-00995-6	Sequence 6, Appli
9	582	43.5	306	US-08-696-139-4	Sequence 4, Appli
10	582	43.5	404	US-08-696-139-2	Sequence 2, Appli
11	567	42.4	329	US-09-011-769A-51	Sequence 51, Appli
12	567	42.4	349	US-09-011-769A-47	Sequence 47, Appli
13	567	42.4	415	US-08-860-882A-57	Sequence 57, Appli
14	567	42.4	415	US-09-011-769A-39	Sequence 39, Appli
15	567	42.4	424	US-09-011-769A-56	Sequence 56, Appli
16	561	41.9	417	US-07-649-591B-7	Sequence 7, Appli
17	561	41.9	417	US-08-277-540-7	Sequence 7, Appli
18	561	41.9	417	US-08-430-787A-7	Sequence 7, Appli
19	560	41.9	349	US-09-011-769A-60	Sequence 60, Appli
20	559	41.8	349	US-09-011-769A-64	Sequence 64, Appli
21	554	41.4	396	US-07-649-591B-4	Sequence 4, Appli
22	554	41.4	396	US-08-277-540-4	Sequence 4, Appli
23	554	41.4	396	US-08-430-787A-4	Sequence 4, Appli
24	552	41.3	417	US-07-649-591B-6	Sequence 6, Appli
25	552	41.3	417	US-08-277-540-6	Sequence 6, Appli
26	552	41.3	417	US-08-430-787A-6	Sequence 6, Appli
27	549	41.0	437	US-09-675-305-10	Sequence 10, Appli

28	549	41.0	613	4	US-09-171-945-113	Sequence 113, App
29	549	41.0	716	4	US-09-171-945-125	Sequence 125, App
30	542	36.8	399	4	US-09-710-099-8	Sequence 8, Appli
31	487.5	36.4	419	1	US-07-649-591B-5	Sequence 5, Appli
32	487.5	36.4	419	1	US-08-277-540-5	Sequence 5, Appli
33	487.5	36.4	419	1	US-08-430-787A-5	Sequence 5, Appli
34	483	36.1	417	1	US-07-649-591B-8	Sequence 8, Appli
35	483	36.1	417	1	US-08-277-540-8	Sequence 8, Appli
36	483	36.1	417	1	US-08-430-787A-8	Sequence 8, Appli
37	471.5	35.2	350	4	US-09-675-305-12	Sequence 12, Appli
38	465.5	34.8	419	4	US-08-640-906-2	Sequence 2, Appli
39	465.5	34.8	419	4	US-09-395-936-2	Sequence 2, Appli
40	465.5	34.8	436	4	US-09-710-099-6	Sequence 6, Appli
41	460.5	34.4	419	4	US-08-640-906-17	Sequence 17, Appli
42	460.5	34.4	419	4	US-09-395-936-17	Sequence 17, Appli
43	459	34.3	417	4	US-08-640-906-4	Sequence 4, Appli
44	459	34.3	417	4	US-09-395-936-4	Sequence 4, Appli
45	458	34.2	417	4	US-08-640-906-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-2
Sequence 2, Application US/09813133A
Patent No. 6455294
GENERAL INFORMATION:
APPLICANT: GAN, Weintu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
FILE REFERENCE: CLO01173
CURRENT FILING DATE: 2001-06-06
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 386
TYPE: PRT
ORGANISM: Human
US-09-813-133A-2

Query Match 93.9%; Score 1257; DB 4; Length 386;
Best Local Similarity 99.1%; Pred. No. 7.4e-129;
Matches 230; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASASYEQYHSLNIEYSMIEFTTERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 60
DB 115 ASASYEQYHSLNIEYSMIEFTTERHPDMLTKIHGSSFEKYPLYVLKVSKEQTAKNAI 174
QY 61 WIDCIIHAREMISPAFCMLFTHGNMRRKNSFYANNICIGTDLNRNASKHMCCEGASS 120
DB 175 WIDCIIHAREMISPAFCMLFTHGNMRRKNSFYANNICIGTDLNRNASKHMCCEGASS 234
QY 121 SSCSETTYGLVPESPEPKAVAFLLRNINQIKAVISMSYSQHTVFPYSYTRSKDHE 180
DB 225 SSCSETTYGLVPESPEPKAVAFLLRNINQIKAVISMSYSQHTVFPYSYTRSKDHE 294
QY 181 ELISLVAEAVRAIEKTSKNTRYTHGSGSETLYLADGGDDWYDGLGIRYSFT 232
DB 295 ELISLVAEAVRAIEKTSKNTRYTHGSGSETLYLADGGDDWYDGLGIRYSFT 346

RESULT 2
US-07-649-591B-3
Sequence 3, Application US/07649591B
Patent No. 5206161
GENERAL INFORMATION:
APPLICANT: Dennis Drayna and Daniel Eaton
TITLE OF INVENTION: NO. 5206161el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649,591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-649-591B-3

Query Match
Best Local Similarity 92.6%; Score 1239.5; DB 1; Length 423;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

1 ASASYEQYHSLNEIYSWIEFTTERHPDMLTKIHGSSFEKYPYLVLKVSKEQYAKNAI 60
115 ASASYEQYHSLNEIYSWIEFTTERHPDMLTKIHGSSFEKYPYLVLKVSKEQYAKNAI 174

61 WIDCGIHAREWISPAFCMLFIGH----- 83
175 WIDCGIHAREWISPAFCMLFIGHITQFYGIQYTNLRLVDFYVMPVNVNDGYDSMKK 234

84 NMMWRKNSFYANNHCIGTDLNRNFASKHWCCEGASSSCSEFTYCGLYPESEPEYKAVAS 143
235 NMMWRKNSFYANNHCIGTDLNRNFASKHWCCEGASSSCSEFTYCGLYPESEPEYKAVAS 294

144 FLRRNINQIKAVISMHSYQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
295 FLRRNINQIKAVISMHSYQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

204 HGHGSETLYLAPGGDDWIYDGIKYSFT 232
355 HGHGSETLYLAPGGDDWIYDGIKYSFT 383

Db

RESULT 3
US-08-277-540-3
Sequence 3, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/277,540
FILING DATE: 19-JUL-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-277-540-3

Query Match
Best Local Similarity 92.6%; Score 1239.5; DB 1; Length 423;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

1 ASASYEQYHSLNEIYSWIEFTTERHPDMLTKIHGSSFEKYPYLVLKVSKEQYAKNAI 60
115 ASASYEQYHSLNEIYSWIEFTTERHPDMLTKIHGSSFEKYPYLVLKVSKEQYAKNAI 174

61 WIDCGIHAREWISPAFCMLFIGH----- 83
175 WIDCGIHAREWISPAFCMLFIGHITQFYGIQYTNLRLVDFYVMPVNVNDGYDSMKK 234

84 NMMWRKNSFYANNHCIGTDLNRNFASKHWCCEGASSSCSEFTYCGLYPESEPEYKAVAS 143
235 NMMWRKNSFYANNHCIGTDLNRNFASKHWCCEGASSSCSEFTYCGLYPESEPEYKAVAS 294

144 FLRRNINQIKAVISMHSYQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 203
295 FLRRNINQIKAVISMHSYQHIIVFPYSYTRSKSKDHEELSLVASEAVRAIEKTSKNTRYT 354

204 HGHGSETLYLAPGGDDWIYDGIKYSFT 232
355 HGHGSETLYLAPGGDDWIYDGIKYSFT 383

Db

RESULT 4
US-08-430-787A-3
Sequence 3, Application US/08430787A
Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Eaton, Dan L.
TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

```
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,787A
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/277,540
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-430-787A-3
```

```
Query Match          92.6%; Score 1239.5; DB 1; Length 423;
Best Local Similarity 86.2%; Pred. No. 6.9e-127;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;
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QY 1 ASASYEQYHSLNFIYMIETFRHPDMLTKIHGSSFEKPYLYLVKVGKEQTANAI 60
    |||||||
DB 115 ASASYEQYHSLNFIYMIETFRHPDMLTKIHGSSFEKPYLYLVKVGKEQTANAI 174

QY 61 WIDCGIHAREWISPAFLMFIH-----83
    |||||||
DB 175 WIDCGIHAREWISPAFLMFIHITQFYGIITQYTNLRLVDFVMPVWVNDGYSMKK 234

QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSEYTCGLYPESEPEVKA 143
    |||||||
DB 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSEYTCGLYPESEPEVKA 294

QY 144 FLRRNIQIKAYISMHSYQIHPYVSYTRSKSKDHLELSVASEAVRALEKTSKNR 203
    |||||||
DB 295 FLRRNIQIKAYISMHSYQIHPYVSYTRSKSKDHLELSVASEAVRALEKTSKNR 354

QY 204 HGHGSETLYLAPGGDDMIYDLGIKYSFT 232
    |||||||
DB 355 HGHGSETLYLAPGGDDMIYDLGIKYSFT 383
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```
RESULT 5
US-08-869-057-2
; Sequence 2, Application US/08869057
; Patent No. 5985562
; GENERAL INFORMATION:
; APPLICANT: Morser, Michael J
; TITLE OF INVENTION: Method of Detecting Thrombotic Disease
; TITLE OF INVENTION: Risk
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Berlex Biosciences Legal Department
; STREET: 15049 San Pablo Avenue
```

```
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804-0099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,057
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Washlien, Wendy L.
REGISTRATION NUMBER: 36,301
REFERENCE/DOCKET NUMBER: 51509AUSM1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-262-5411
TELEFAX: 510-262-7095
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE: Plasma
TISSUE TYPE:
FEATURE:
NAME/KEY: Peptide
LOCATION: 23..401
US-08-869-057-2
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Query Match          92.6%; Score 1239.5; DB 2; Length 423;
Best Local Similarity 86.2%; Pred. No. 6.9e-127;
Matches 232; Conservative 0; Mismatches 0; Indels 37; Gaps 1;
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QY 1 ASASYEQYHSLNFIYMIETFRHPDMLTKIHGSSFEKPYLYLVKVGKEQTANAI 60
    |||||||
DB 115 ASASYEQYHSLNFIYMIETFRHPDMLTKIHGSSFEKPYLYLVKVGKEQTANAI 174

QY 61 WIDCGIHAREWISPAFLMFIH-----83
    |||||||
DB 175 WIDCGIHAREWISPAFLMFIHITQFYGIITQYTNLRLVDFVMPVWVNDGYSMKK 234

QY 84 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSEYTCGLYPESEPEVKA 143
    |||||||
DB 235 NRMWRKNRSFYANNHCIGTDLNRFASKHWCCEGASSSCSEYTCGLYPESEPEVKA 294

QY 144 FLRRNIQIKAYISMHSYQIHPYVSYTRSKSKDHLELSVASEAVRALEKTSKNR 203
    |||||||
DB 295 FLRRNIQIKAYISMHSYQIHPYVSYTRSKSKDHLELSVASEAVRALEKTSKNR 354

QY 204 HGHGSETLYLAPGGDDMIYDLGIKYSFT 232
    |||||||
DB 355 HGHGSETLYLAPGGDDMIYDLGIKYSFT 383
```

```
RESULT 6
US-09-813-133A-4
; Sequence 4, Application US/09813133A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, Weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, AND
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1001173
; CURRENT APPLICATION NUMBER: US/09/813,133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
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SEQ ID NO 4
LENGTH: 423
TYPE: PRT
ORGANISM: Human
US-09-813-133A-4

Query Match 91.8%; Score 1228.5; DB 4; Length 423;
Best Local Similarity 85.5%; Pred. No. 1.1e-125;
Matches 230; Conservative 0; Mismatches 2; Indels 37; Gaps 1;

QY 1 ASASYEQYHSLNETYSWIEFTEHRPDMLTRIHIGSFEEKYPLYLVKSGKEQTAKNAI 60
DB 115 ASASYEQYHSLNETYSWIEFTEHRPDMLTRIHIGSFEEKYPLYLVKSGKEQTAKNAI 174
QY 61 WIDCGIHAREWISPAFCMLFIGH-----83
DB 175 WIDCGIHAREWISPAFCMLFIGHITQIFGIQOTNLRLVDYFVYVNVNDGYSMKK 234
QY 84 NRMWRKNSFYANNHCIGTDLNRNFASKHMCCEGASSSCSEYCYGLYPESEPEYKAVAS 143
DB 235 NRMWRKNSFYANNHCIGTDLNRNFASKHMCCEGASSSCSEYCYGLYPESEPEYKAVAS 294
QY 144 FLRRINQIKAYISMHSYSHQHYFVYSTRSKSKDHELSLVASEAVRAIEKTSKNTRYT 203
DB 295 FLRRINQIKAYISMHSYSHQHYFVYSTRSKSKDHELSLVASEAVRAIEKTSKNTRYT 354
QY 204 HGHGSETLYLAPGGGDDMIYDLGIKYSFT 232
DB 355 HGHGSETLYLAPGGGDDMIYDLGIKYSFT 383

RESULT 7

US-08-782-760-6
Sequence 6, Application US/08782760
Patent No. 5948668

GENERAL INFORMATION:
APPLICANT: Hartman, Jacob
APPLICANT: Fulga, Netta
APPLICANT: Mendelovitch, Simona
APPLICANT: Gorecki, Marian
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,760
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,233
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0336/43847
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 307 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-782-760-6

Query Match 45.6%; Score 610; DB 2; Length 307;
Best Local Similarity 45.0%; Pred. No. 2.2e-58;
Matches 121; Conservative 43; Mismatches 65; Indels 40; Gaps 5;

QY 1 ASASYEQYHSLNETYSWIEFTEHRPDMLTRIHIGSFEEKYPLYLVKSGKEQTAKNAI 60
DB 1 ASGHSTYNNWETIEAMIQVATNDPNLDLYQSVIGTFEGRNMYLKI-GKTRPNKPAI 59
QY 61 WIDCGIHAREWISPAFCMLFIGH-----83
DB 60 FIDCGIHAREWISPAFCMLFIGHREAVRYNOELHMKQLDELDFVLPVNVINDGVYTWTK 119
QY 84 NRMWRKNSFYANNHCIGTDLNRNFASKHMCCEGASSSCSEYCYGLYPESEPEYKAVAS 143
DB 120 DRMRKTRSTWAGSSCGLVDPNRF-NAGCEYVASRSPSEYCYGAPSEKETAKLAD 178
QY 144 FLRRINQIKAYISMHSYSHQHYFVYSTRSKSKDHELSLVASEAVRAIEKTSKNTRYT 203
DB 179 FIRNLSITIKAYLIHSYQWMLYPYDYKLPENYELNALVYGAKEI-ATLHGTRKYT 237
QY 204 HGHGSETLYLAPGGGDDMIYDLGIKYSFT 232
DB 238 YGPGATITTYPAAGSSDDWSTIDGIKYSFT 266

RESULT 8

PCT-US96-00995-6
Sequence 6, Application PC/TUS9600995
Patent No. 5948668

GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00995
FILING DATE: 25-JAN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 308 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-00995-6

Query Match 45.6%; Score 610; DB 5; Length 307;
Best Local Similarity 45.0%; Pred. No. 2.2e-58;
Matches 121; Conservative 43; Mismatches 65; Indels 40; Gaps 5;

QY 1 ASASYEQYHSLNETYSWIEFTEHRPDMLTRIHIGSFEEKYPLYLVKSGKEQTAKNAI 60

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DB 1 ASGHSTTKYNNMETEAMTQVATDNDPLVQSVIGTTEGRNMYLKI-GKTRPNKPAI 59
QY 61 WIDCGIHAREWISPAFLMEI-----GH-----83
DB 60 FIDCGHAREWISPAFCQFVREAVTYNOELHMKLDELDFYLPVYNIDCYVTWTWK 119
QY 84 NRMWRKRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVAS 143
DB 120 DRMRKTRSTMGSSCLGVDPNRNF-NAGWCVEGASRSCSEYCGPAPSEKETALAD 178
QY 144 ELRRNINOKATISMHSYQHIYFPIYSTRSKSKDHEELSLVASEAVRAIKTSKTRIT 203
DB 179 FIRNNISTIKAVLTIHYSQOMILYPSYDYKLPENYEELNALVKGAKEI-ATLHGTXYT 237
QY 204 HGHSEELVAPGGDDWIYDLGIRKYSFT 232
DB 238 YCGGATTIYPAGGSDDMYSIDGIRKYSFT 266
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RESULT 9

```
US-08-696-139-4
; Sequence 4, Application US/08696139
; Patent No. 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hersberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Steiner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-696-139-4
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Query Match 43.5%; Score 582; DB 1; Length 306;
Best Local Similarity 44.3%; Pred. No. 2.5e-55;
Matches 117; Conservative 40; Mismatches 67; Indels 40; Gaps 5;
QY 6 YEOYHSLNELYSWIEFTTERHPDMLTKIHIGSFEKYPPLYLVKSGKEQTAKNAIWDG 65
```

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DB 6 YEKYNNMETEAMTKQVTSNPDLISRAIGTFIGNNITYLLKV-GKPPNKPALFMDG 64
QY 66 IHAREWISPAFLMEI-----GH-----NRMWR 88
DB 65 FHAREWISPAFCQFVREAVLYGYSHMTPELNKIDFVLPVYNIDCYVTWTWK 124
QY 89 KRSFYANNHCIGTDLNRNFASKHWCCEGASSSCSETYCGLYPESEPEVKAVASFLRRN 148
DB 125 KTRSTMGSSCLGVDPNRNF-DAGWCCTGTGASTDPCDEYCGSAESEKETALADFI 183
QY 149 INOKATISMHSYQHIYFPIYSTRSKSKDHEELSLVASEAVRAIKTSKTRITGHGS 208
DB 184 LSSIKAVLTIHYSQOMILYPSYDYKLPENYELNALVKAAMEL-ATLYGTXYTYPGA 242
QY 209 ETLVAPGGDDWIYDLGIRKYSFT 232
DB 243 TTIYPAGGSDDMYIDGIRKYSFT 266
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RESULT 10

```
US-08-696-139-2
; Sequence 2, Application US/08696139
; Patent No. 5672496
; GENERAL INFORMATION:
; APPLICANT: Fayerman, Jeffrey T.
; APPLICANT: Greenen, David P.
; APPLICANT: Hersberger, Charles L.
; APPLICANT: Larson, Jeffrey L.
; APPLICANT: Steiner, Jane L.
; APPLICANT: Zhang, Haichao
; TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
; TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States of America
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,139
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,258
; FILING DATE: 16-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaylo, Paul J.
; REGISTRATION NUMBER: 36,808
; REFERENCE/DOCKET NUMBER: X-8681
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0756
; TELEFAX: (317) 276-3861
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 404 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-696-139-2
```

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Query Match 43.5%; Score 582; DB 1; Length 404;
Best Local Similarity 44.3%; Pred. No. 3.8e-55;
Matches 117; Conservative 40; Mismatches 67; Indels 40; Gaps 5;
QY 6 YEOYHSLNELYSWIEFTTERHPDMLTKIHIGSFEKYPPLYLVKSGKEQTAKNAIWDG 65
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Db 104 YEKYNNMETIEAMTKQVYSENPDLISFALGTFELGNNIYLKV-GKGGPKKPAIFMCG 162
Y 66 IHAEMWISPAFCIMFT-----GH-----NRMR 88
Db 163 FHAREWISHACQWVREAVRTYRGREIQTVELDLDFVLPVINDGYITWTKNRMR 222
Y 89 KNRSEYANNHCIGTDLNRFASKHWCCEGASSSCSEFTYCGLYPESEPEKAVASFLRN 148
Db 223 KTRSTNACTTCIGTDPNNF-DAGCTTGASTDPCDETYCCSAASEKETKALADFLRN 281
Y 149 INQIAVYISMHSQIHVPEYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYTHGHS 208
Db 282 LSSIAVYLIHSYSQMIYPYSYDKLENNALNLAKAAYKEL-ATLYGTKTYGPGA 340
Y 209 ETLVAPGGDDMIYDLGIRKSYFT 232
Db 341 TTTPAAGSDDMWAYDQGIKSYFT 364

RESULT 11
US-09-011-769A-51

; Sequence 51, Application US/09011769A
; Patent No. 643691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKEY, David C.

DAVIES, David H.

HENNAM, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 329 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 51:

US-09-011-769A-51

Query Match 42.4%; Score 567; DB 4; Length 329;

Best Local Similarity 41.3%; Pred. No. 1.2e-53;

Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Y 1 ASASYEQYHSLNELYSWIEFTERRHPDMLTKIHGSSFEKYPVLYLVKVSKEQTAKNAI 60

Db 23 ATGSHYKYNKMETIEAMTKQVATENPALISRVIGTFEGRAIYLKV-GKAGQKPAI 81
Y 61 WIDCGIHAREWISPAFCIMFT-----GH-----NRMR 83
Db 82 FMDCGFHAREWISPAFCQWVREAVRTYRGREIQTVELDLDFVLPVINDGYITWTK 141
Y 84 NNRMRKRSYANNHCIGTDLNRFASKHWCCEGASSSCSEFTYCGLYPESEPEKAVAS 143
Db 142 SRFMRKTRSTHTGSSCIGTDPNNF-DAGWCEIGASRNPDCDETYCCPAASEKETKALAD 200
Y 144 FLRRNQIAVYISMHSQIHVPEYSTRSKSDHEELSLVASEAVRAIEKTSKNTRYT 203
Db 201 FIRKLSSIAVYLIHSYSQMIYPYSYDKLENNALNLAKAAYKEL-ASLHGTYT 259
Y 204 HGHGSETLVAPGGDDMIYDLGIRKSYFT 232
Db 260 YGPGATTVTPAAGSDDMWAYDQGIKSYFT 288

RESULT 12
US-09-011-769A-47

; Sequence 47, Application US/09011769A
; Patent No. 643691

GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.

BLAKEY, David C.

DAVIES, David H.

HENNAM, John F.

HENNEQUIN, Laurent F.A.

MARSHAM, Peter R.

DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds

NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, LLP

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 9611019.2

FILING DATE: 25-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 47:

US-09-011-769A-47

Query Match 42.4%; Score 567; DB 4; Length 349;

Best Local Similarity 41.3%; Pred. No. 1.3e-53;

Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Y 1 ASASYEQYHSLNELYSWIEFTERRHPDMLTKIHGSSFEKYPVLYLVKVSKEQTAKNAI 60

Db 23 ATGSHYKYNWETIEATQVATENPALISRVIGTFEGRAIYLKV-GKAGONKPAI 81
Qy 61 WIDGIAHREWISPAFCIMFT-----GH----- 83
Db 82 FMDGCFHAREWISPAFCIMFT-----GH----- 83
Qy 84 NRMKRNSFPANNHCICTDLNRNFASKHMCCEGASSSSCSEYTCGLYPESEPEVKAVAS 143
Db 142 SRFWKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAESEKETKALAD 200
Qy 144 FLRRNINOIKAYISMHSYQHIIVEPYSTRSKSKDHEELSLVASEAVRAIKTSKNTRYT 203
Db 201 FIRKLSSIKAYLTIHSYSQMMIYPSYAYKLGEMNMLAKATVKEL-ASLHGTYT 259
Qy 204 HGHGETIYLA PGDDMIYDLGIKYSFT 232
Db 260 YPGATTIYPAGGSDDWADOGIRYSFT 288

RESULT 13

US-08-860-882A-57
Sequence 57, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HUM
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-860-882A-57

Query Match 42.4%; Score 567; DB 2; Length 415;
Best Local Similarity 41.3%; Pred. No. 1.7e-53;
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

Qy 1 ASASYEQHSLNELYSMWIEFFTERHPDLTKIHGSSFEKYPLVYLKSGEQTAKNAI 60
Db 109 ATGSHYKYNWETIEATQVATENPALISRVIGTFEGRAIYLKV-GKAGONKPAI 167
Qy 61 WIDGIAHREWISPAFCIMFT-----GH----- 83
Db 168 FMDGCFHAREWISPAFCIMFT-----GH----- 83
Qy 84 NRMKRNSFPANNHCICTDLNRNFASKHMCCEGASSSSCSEYTCGLYPESEPEVKAVAS 143
Db 228 SRFWKTRSTHTGSSCIGTDPNRNF-DAGWCEIGASRNPCDETYCGPAESEKETKALAD 286
Qy 144 FLRRNINOIKAYISMHSYQHIIVEPYSTRSKSKDHEELSLVASEAVRAIKTSKNTRYT 203
Db 287 FIRKLSSIKAYLTIHSYSQMMIYPSYAYKLGEMNMLAKATVKEL-ASLHGTYT 345
Qy 204 HGHGETIYLA PGDDMIYDLGIKYSFT 232
Db 346 YPGATTIYPAGGSDDWADOGIRYSFT 374

RESULT 14

US-09-011-769A-39
Sequence 39, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
APPLICANT: BLAKELY, David C.
APPLICANT: DAVIES, David H.
APPLICANT: HENNAM, John F.
APPLICANT: HENNEQUIN, Laurent F.A.
APPLICANT: MARSHAM, Peter R.
APPLICANT: DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-011-769A-39

Query Match 42.4%; Score 567; DB 4; Length 415;
Best Local Similarity 41.3%; Pred. No. 1.7e-53;
Matches 111; Conservative 46; Mismatches 72; Indels 40; Gaps 5;

[illegible]

RESULT 15
US-09-011

```

? Sequence 56, Application US/09011769A
? Patent No. 6436691
? GENERAL INFORMATION:
? APPLICANT: SLATER, Anthony M.,
? BLANEY, David C.,
? DAVIES, David H.,
? HENNAM, John F.,
? HENNEQUIN, Laurent F.A.,
? MARSHAM, Peter R.,
? DOWELL, Robert I.,
? TITLE OF INVENTION: Chemical Compounds
? NUMBER OF SEQUENCES: 87
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pillsbury Madison & Sutro, LLP
? STREET: 1100 New York Ave., N.W.,
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 1.44 Mb disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: MS Word
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/011,769A
? FILING DATE: 13-Feb-1998
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/GB96/01975
? FILING DATE: 13-AUG-1996
? APPLICATION NUMBER: GB 9612295.7
? FILING DATE: 12-JUN-1996
? APPLICATION NUMBER: GB 9611019.2
? FILING DATE: 25-MAY-1996
? APPLICATION NUMBER: GB 9516810.0
? FILING DATE: 16-AUG-1995
? INFORMATION FOR SEQ ID NO: 56:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 424 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 56:
? IS-09-011-769A-56

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Query Match	42.48;	Score 567;	DB 4;	Length 424;
Best Local Similarity	41.38;	Pred. No. 1.8e-53;		
Matches 111; Conservative	46;	Mismatches 72;	Indels 40;	Gaps 5

OY	1	AASAYEDYHSLNELYNSIEETTERHPMLKIHGSSFEKYPLYVLKSKEOTAKNAI	60
Dd	118	ATGHSEYEKNKWETLEAMTOQVALENPALISRSVIGTTFEGRAITYLLKV-GKAQONKPAI	170
OY	61	WIDDCIHAREMISPACLMFT-----GH-----	83
Dd	177	FMDCGFAHREMIISPAFCOMFVEARVTYGRELOVELDKLDFEVLPLINDIGIYTMTK	233
OY	84	NRMNRKNSFWANHHCTGDJDNRAFASKHWCEEGASSSGSETGYCGLYPESEPVRKVAS	143
Dd	237	SREMRKRSTHTTGSSCIOTDPNNRF-DAGWCETIASRNPDETYTCGRAESEKTKTLAD	293
OY	144	FLRRNIINIKAYISMHSYQHIVEPYSYTRNSKDHDELIVASEAVARALETSKNTRYT	203
Dd	296	FIRKLISKIKAYLTIIHYSQMMIIPYSAVKYLGENNAELNALAKATVKEL-ASLHGTRYT	353
OY	204	HGHSSETLYLAPGGGDDMIYDLGIKYSTP	232
Dd	355	YGPQATTITYPAGGSDDAWDYGILRYSTP	383

Search completed: May 12, 2003, 09:17:48
Job time : 11.3814 secs

Job time : 11.3814 secs

GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 03:14:57 ; Search time 35.0847 seconds
(without alignments)
3146.770 Million cell updates/sec

Title: US-09-980-881A-2
Perfect score: 1911
Sequence: 1 MKLSTLAVLVPIVLECEQHV.....IKSFTSNPVEKLLPLSLK 360

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 seqs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O/cgn2.1/uspro.spool/US09980881/runat.12052003_085041.16630/app_query.fasta.1.1429
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09980881@cgn.1.1.62 @runat.12052003_085041.16630 -NCPU=6 -ICPU=3
-NO_XLPHY -NO_MMAP -LARGEIOERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMECOUT=120
-WARN_TIMECOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued_Patents_NA:*

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- 3: /cgn2.6/prodata/1/lna/6a.COMB.seq:*
- 4: /cgn2.6/prodata/1/lna/5b.COMB.seq:*
- 5: /cgn2.6/prodata/1/lna/PCTUS.COMB.seq:*
- 6: /cgn2.6/prodata/1/lna/backfiles1.seq:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1849.5	96.8	1625	4 US-09-813-133A-1	Sequence 1, Appl1
2	1832	95.9	1272	2 US-08-869-057-1	Sequence 1, Appl1
3	1832	95.9	1749	1 US-07-649-591B-2	Sequence 2, Appl1
4	1832	95.9	1749	1 US-08-277-540-2	Sequence 2, Appl1
5	1832	95.9	1749	1 US-08-430-282A-2	Sequence 2, Appl1
6	640.5	33.5	1215	1 US-08-696-139-1	Sequence 1, Appl1
7	639	33.4	1263	2 US-08-860-882A-56	Sequence 56, Appl1
8	639	33.4	1263	4 US-09-011-769A-38	Sequence 38, Appl1
9	631.5	33.0	1284	2 US-08-860-882A-71	Sequence 71, Appl1
10	631.5	33.0	1284	4 US-09-011-769A-55	Sequence 55, Appl1
11	623	32.6	2154	4 US-09-171-945-124	Sequence 124, Appl1
12	611.5	32.0	1311	4 US-09-675-305-9	Sequence 9, Appl1

13	604	31.6	927	2 US-08-782-760-5	Sequence 5, Appl1
14	604	31.6	927	5 PCT-US96-00995-5	Sequence 5, Appl1
15	576	30.1	921	1 US-08-696-139-3	Sequence 3, Appl1
16	564	29.5	2128	4 US-09-675-305-13	Sequence 13, Appl1
17	561	29.4	999	2 US-08-860-882A-67	Sequence 67, Appl1
18	561	29.4	999	4 US-09-011-769A-50	Sequence 50, Appl1
19	561	29.4	1053	2 US-08-860-882A-64	Sequence 64, Appl1
20	561	29.4	1053	4 US-09-011-769A-46	Sequence 46, Appl1
21	554	29.0	1059	2 US-08-860-882A-74	Sequence 74, Appl1
22	554	29.0	1059	4 US-09-011-769A-59	Sequence 59, Appl1
23	553	28.9	1059	2 US-08-860-882A-77	Sequence 77, Appl1
24	553	28.9	1059	4 US-09-011-769A-63	Sequence 63, Appl1
25	546	28.6	1200	4 US-09-710-099-7	Sequence 7, Appl1
26	543	28.4	1870	4 US-09-171-945-112	Sequence 112, Appl1
27	528.5	27.7	1050	4 US-09-675-305-11	Sequence 11, Appl1
28	519.5	27.2	1311	4 US-09-710-099-5	Sequence 5, Appl1
29	513	26.8	1251	3 US-08-640-906-3	Sequence 3, Appl1
30	513	26.8	1251	4 US-09-395-936-3	Sequence 3, Appl1
31	487.5	25.5	1257	3 US-08-640-906-1	Sequence 1, Appl1
32	487.5	25.5	1257	4 US-09-395-936-1	Sequence 1, Appl1
33	460.5	24.1	945	4 US-09-710-099-3	Sequence 3, Appl1
34	460.5	24.1	945	4 US-09-710-099-11	Sequence 11, Appl1
35	458.5	24.0	2247	4 US-09-710-099-15	Sequence 15, Appl1
36	434	22.7	1056	4 US-09-710-099-7	Sequence 7, Appl1
37	434	22.7	1056	4 US-09-710-099-9	Sequence 9, Appl1
38	363	19.0	55827	4 US-09-813-133A-3	Sequence 3, Appl1
39	289.5	15.1	741	4 US-09-675-305-5	Sequence 5, Appl1
40	213	11.1	591	4 US-09-331-709-2	Sequence 2, Appl1
41	198.5	10.4	629	4 US-09-280-116-228	Sequence 228, Appl1
42	168.5	8.8	515	4 US-08-998-416-125	Sequence 125, Appl1
43	133.5	7.0	673	4 US-09-280-116-93	Sequence 93, Appl1
44	118.5	6.2	2504	1 US-08-484-105-15	Sequence 15, Appl1
45	118.5	6.2	2504	1 US-08-484-106-15	Sequence 15, Appl1

ALIGNMENTS

RESULT 1
US-09-813-133A-1
; Sequence 1, Application US/0981333A
; Patent No. 6455294
; GENERAL INFORMATION:
; APPLICANT: GAN, weiniu et al
; TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
; FILE REFERENCE: C1001173
; CURRENT APPLICATION NUMBER: US/09/813.133A
; CURRENT FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1625
; TYPE: DNA
; ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

pred. No.: 1 99e-221 Length: 1625
Score: 1849.50 Matches: 355
Percent Similarity: 94.18% Conservative: 1
Best Local Similarity: 93.92% Mismatches: 4
Query Match: 96.78% Indels: 18
DB: Gaps: 1

US-09-980-881A-2 (1-360) x US-09-813-133A-1 (1-1625)

QY 1 MetLysLeuCySserLeuAlaValLeuValProIleValLeuPheCySGluGlnHisVal 20
Db 17 ATGAAGCTTTCACACCTTCAGCTCTGTACCAATGTTCTCTGTGACACAGTTC 76
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaAlaLeuProAlaGlyThrSerArgGlnValGln 40
|||||

Db 77 TTCGGCTTCAGAGTGGCCAACTTCTAGCTGCTTCTCCAGAACCTTACGCAAGTTCGA 136
QY 41 ValLeuGlnAsnLeuThrThrThyTyrGluIleValLeuTyrGlnProValThrAlaasp 60
Db 137 GTTCTACGAACTTCTACACATATGATGATTTCTCTGACACCGGTACACACTGC 196
QY 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValaspVal 80
Db 197 CTTATTGGAGAAAAAACAACTCATTTTGTGTAATGCATCTGATGTCACATGTG 256
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaaspValasp 100
Db 257 AAAGCCCATTTAAATGATGAGCGGCAATTCACATGCTGCTGCGAGATGCGAAGAT 316
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyr 120
Db 317 CTTATTCAACAGCAGATTTCCACACACAGTACAGCCCCGCGCTCCGCACTGACTAT 376
QY 121 GlnGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheIleGluPheIleThrGlnArgHis 140
Db 377 GAACAGTATCACTCACTAAATGAATCTATTCTTGATAGAAATTAATACAGAGAGCAT 436
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 437 CCGATATGCTTACAAAATCCACATTTGATTCCTCATTTGAGAAATACCCACTATGTT 496
QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheIleAspCysGlyIle 180
Db 497 TTTAAAGTTTCTGGAAAGAACACACACCAAAATGCCATATGATGATGACTGTGGAATC 556
QY 181 HisAlaArgGluTyrPheIleSerProAlaPheCysLeuTyrPheIleGlyHisAsnArgMet 200
Db 557 CATGCCAGAGATGATGATCTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 616
QY 201 TrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSer 220
Db 617 TGGAGAAAGAACCGTTCTTTCTATGCGAACATCTTCTCATGCGAGACGACCTGGAATAG 676
QY 221 AsnPheValSerLysHisIleTyrCysGluGlnIleLysAlaSerSerSerCysSerGluThr 240
Db 677 AACTTCTGCTTCCAAACACGCTGTGAGAGAGTGCATCTCATCTCTCATCTGCGAAACC 736
QY 241 TyrCysGlyLeuTyrProGlnSerGluProGlnValLysAlaValAlaSerPheLeuArg 260
Db 737 TACTGTGACTTATCCGAGTCAAGAACCAAGTGAAGGAGTGGCTGCTGCTGCTGCTGCTG 796
QY 261 ArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleVal 280
Db 797 AGAATATCAACGACGATTAAGCATACATCAGCATGCTTCTATCTCCACACATATAGTG 856
QY 281 PheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlnLeuSerLeuValAla 300
Db 857 TTTCCATATCTCTATACAGCAAGTAAAGCAAGACCATGAGAACTGCTCTGTAAGCC 916
QY 301 SerGlnIleValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHis 320
Db 917 AGTAAGCAAGTCTGTCTATTTAGAGAAATTAATAAATACAGATATACACAGGCGCAT 976
QY 321 GlySerGlnThrLeuTyrLeuAlaProGlyGlyLysAspSerTyrPheIleTyrAspLeuGly 340
Db 977 GGCCTCAAGAACCTTATACCTAGCTCTCTGAGAGTGGGACCATTTGATCTATGATTTGGGC 1036
QY 341 IleLysTyrSerPhe----- 345
Db 1037 ATCAAAATATTGTTACAAATGAACTTCGAGATACGGGCAATACGATTTCTGCTGCGG 1096
QY 346 -----ThSerSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1097 GAGCGTTACATCAAAACCCACCTGTAGAGAGCTTTTCCGCTGCTCTATAAA 1148
RESULT 2
US-08-869-057-1
Sequence 1, Application US/08869057

Patent No. 5985562
GENERAL INFORMATION:
APPLICANT: Moiser, Michael J
APPLICANT: Nagashima, Mariko
TITLE OF INVENTION: Method of Detecting Thrombotic Disease
TITLE OF INVENTION: Risk
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Berlex Biosciences Legal Department
STREET: 15049 San Pablo Avenue
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804-0099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/869,057
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Washlien, Wendy L
REGISTRATION NUMBER: 36,301
REFERENCE/DOCKET NUMBER: 51509AUSM1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-262-5411
TELEFAX: 510-262-7095
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
PUBLICATION INFORMATION:
AUTHORS: Eaton, Dan L.
AUTHORS: Malloy, Beth E.
AUTHORS: Tsai, Siao P.
AUTHORS: Henzel, William
AUTHORS: Drayna, Dennis
TITLE: Isolation, Molecular Cloning, and Partial
TITLE: Characterization of a No. 5985562el Carboxypeptidase B
JOURNAL: J. Biol. Chem.
VOLUME: 266
ISSUE: 32
PAGES: 21833-21838
DATE: No. 5985562 15-1991
US-08-869-057-1
Alignment Scores:
Pred. No.: 2,05e-219 Length: 1272
Score: 1832.00 Matches: 357
Percent Similarity: 86.27% Conservative: 1
Best Local Similarity: 86.02% Mismatches: 55
Query Match: 95.87% Indels: 2
Gaps: 2
US-09-980-881A-2 (1-360) x US-08-869-057-1 (1-1272)
QY 1 MetLysLeuGlnSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 1 ATGAAAGCTTGGACGCTTGACGCTTGTGAACCATTTCTCTCTGTAGAGCAAGATGTC 60
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGln 40
Db 61 TTCGGCTTCAGAGTGGCCAGATTTAGCTGCTTCTCTAGAACCTCTAGGCAAGTTCAA 120
QY 41 ValLeuGlnAsnLeuThrThrThyTyrGluIleValLeuTyrGlnProValThrAlaasp 60

Db 121 GTTCTACAGAACTTCTACTACACATATGAGATTGTCTCTGGCAGCGGTAACAGCTGAC 180
 QY 61 LeuIleValIysLysLysGlnValHisPhePheValAsnAlaSerAspValAlaAspVal 80
 Db 181 CTTATTGTGAAGAAAAACAAGTCCATTTTGTAAATGATCTGATCTGACAATGTG 240
 QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
 Db 241 AAAGCCCATTTAAATGTGAGCGGAATTCATGCTGCTGTGCGCAGACGTGAAGAT 300
 QY 101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProAlaGlnAlaSerTyrTyr 120
 Db 301 CTTATTTCAACAGCAGATTTCACAGACACACTGACCCCGAGCTCCGATCTGACTACT 360
 QY 121 GluGlnIleHisSerLeuAsnGlnIleTyrSerTrpIleGluPheIleThrGluArgHis 140
 Db 361 GAACAGATCATCTACATAAATGAATCTATCTTGATAGATTTATTAACGAGAGCAT 420
 QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
 Db 421 CCGATATGCTTACAAAATCCACATTGATCCCTCATTTGAGAAGTACCCTGATCTT 480
 QY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyLe 180
 Db 481 TTAAGGTTCTGGAAGAAGAACCAACAGCCAAAATGCCATATGATGACTGTGGAATC 540
 QY 181 HisAlaArgIleTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
 Db 541 CATGCCAGAGATGATCTCTCCCTGCTTTCGCTTGCTGCTCATAGGCCATATACTCA 600
 QY 197 197
 Db 601 TTCTATGGCATATAGGGCAATATACCAATCTCTGAGGCTTGCGATTTCTATGTTATG 660
 QY 198 198
 Db 661 CCGGTGTTAATGTGACCGTTATGACTACTCATGAGAAAAGAAATCGATGTGAAG 720
 QY 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
 Db 721 AACGGTCTTTCTATGGAAACAATCATGTCATGGAGAACGCTGAATAGAGAACTTGCT 780
 QY 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerSerSerGluThrTyrCysGly 243
 Db 781 TCCAAACACTGCTGTGGAAGGTGTCATCCAGTTCCTCATCTCGGAAACCTACTGTGA 840
 QY 244 LeuTrpProGluSerGluProGluValIleValAlaIleSerPheLeuArgAsnIle 263
 Db 841 CTTATCTGTGAGTGAACCAAGAGTGAAGCGAGCTGCTAGTTCTTGAGAAAGAAATATC 900
 QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
 Db 901 AACCAATTAAGCATATCATGATGATCATCTCCGCAATATATGCTTTCCATAT 960
 QY 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303
 Db 961 TCCATATACAGCAAGTAAAGCAAGACCATGAGAACGTCTCTAGTACGACGAGAACCA 1020
 QY 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
 Db 1021 GTTGTGCTATGTAAGAAACTAGTAAGAAATACAGGTATACATGCGCATGCGCTCACAGA 1080
 QY 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
 Db 1081 ACCTTATACCTAGCTCTCGAGAGTGGGAGCATGATGATCTATGATTTGGCATCAAAAT 1140
 QY 344 SerPhe 1140
 Db 1141 TCGTTTCAATTGAACCTCGAGATACGGGACATACGGAATCTTGCTGCGGAGCGTTAC 1200
 QY 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
 Db 1201 ATCAAAACCCACCTGTAGAGAGCTTTTGCCTGCTCTCTAATAA 1243

RESULT 3
 US-07-649-591B-2
 : Sequence 2, Application US/07649591B
 : Patent No. 5206161
 :
 : GENERAL INFORMATION:
 : APPLICANT: Dennis Dreyne and Daniel Eaton
 : TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: patin (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/649,591B
 : FILING DATE: 19910201
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hasak, Janet E.
 : REGISTRATION NUMBER: 28,616
 : REFERENCE/DOCKET NUMBER: 689
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/266-1896
 : TELEFAX: 415/952-9881
 :
 : INFORMATION FOR SEQ ID NO: 2:
 :
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1749 bases
 : TYPE: NUCLEIC ACID
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 :
 : FEATURE:
 : NAME/KEY: hybridization probe
 : LOCATION: 133 to 178
 : IDENTIFICATION METHOD:
 : OTHER INFORMATION:
 :
 : FEATURE:
 : NAME/KEY: potential clip site
 : LOCATION: 380 to 382
 : IDENTIFICATION METHOD:
 : OTHER INFORMATION:
 :
 : FEATURE:
 : NAME/KEY: signal sequence
 : LOCATION: 41 to 106
 : IDENTIFICATION METHOD:
 : OTHER INFORMATION:
 :
 : US-07-649-591B-2
 :
 : Alignment Scores:
 : Pred. NO.: 3,51e-219 Length: 1749
 : Score: 1832.00 Matches: 357
 : Percent Similarity: 86.27% Conservative: 1
 : Best local Similarity: 86.02% Mismatches: 2
 : Query Match: 95.87% Indels: 55
 : Gaps: 2
 :
 : US-09-980-881a-2 (1-360) x US-07-649-591B-2 (1-1749)
 :
 : QY 1 MetLysLeuGysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
 : Db 41 ATGAGCTTTCAGCGCTTGACAGTCTGTACCATGTTCTCTGTGAGCAGCATGTG 100

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OY 21 PheAlaPheGlnSerGlyGlnValLeuAlaIleuProArgThrSerArgGlnValGln 40
DB 101 TTCGGGTTTCACAGTGGCCAACTTCTAGCTGCTCTTCTAGAACCTCTTAGCCAACTTCAA 160
OY 41 ValLeuGlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaasp 60
DB 161 GTTCTACAGAACTTCTACACATATGATGATGTTCTCTGCGACCGGTACACCTGCAC 220
OY 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspVal 80
DB 221 CTTATTGTCAGAAAAAACCACTCAATTTTGTGTAATGCTGTGATGTCGACAAATGTG 280
OY 81 LysAlaHisLysAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluasp 100
DB 281 AAAGCCCATTTAAATGATGAGCGGAATTCACATGCTGCTGCGACAGCTGGAAT 340
OY 101 LeuIleGlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
DB 341 CTTATTACACAGCAGATTTCACACACAGCAGCAGCCCGCAGCTCCGATCGTACTAT 400
OY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTyrPheIleThrGluArgHis 140
DB 401 GAACAGTATCTACTCTAAATGAATCTATCTTGATGATGATTAATTAAGTACAGGCAAT 460
OY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
DB 461 CCGTATATGCTTACAAAATCCACATTCGATCCATTTGAGAAAGTACCCTCATGTT 520
OY 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyIle 180
DB 521 TTAAAGGTTTCTGGAAAAAGAAACAAACACCCAAATGCAATGATGATGCTGGATC 580
OY 181 HisAlaArgGluTyrPheLeuSerProAlaPheCysLeuTyrPheIleGlyHis 197
DB 581 CATGCCAGAGATGGATCTCTCCGCTTCTGCTTCTGCTGCTCATAGGCCATATACCTCA 640
OY 197 197
DB 641 TTCATATGGGATTAATAGGCAATATACCAATCTCCTGAGCGTTGTGATTTCTATGTTATG 700
OY 198 198
DB 701 CCGGTGCTTATGTCGACGGTTATGACTACTACTCATGCAAAAAAGATTCGATGTGAGAAAG 760
OY 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
DB 761 AACCGTTCTTCTATGCGAACATCATTCGATTCGGAACAGACCTGAAATAGCACTTGGCT 820
OY 224 SerLysHisTyrCysGluGluGlnLysAlaSerSerSerSerCysSerGluThrTyrCysGly 243
DB 821 TCCAAACACTGGTGTGAGGAAGTGATCCAGTTCCTATGCTGGAACCTACTCTGGA 880
OY 244 LeuTyrProGlnSerGluProGlnValLysAlaValAlaSerPheLeuArgArgAsnIle 263
DB 881 CTTTATCTCTGATGAGAACCAAGCATGAGCACTGGCTAGTCTTCTGAGAACAAATATC 940
OY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
DB 941 AACCAAGTTTAAACATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1000
OY 284 SerTyrThrArgSerLysSerLysAspHisGluGlnLeuSerLeuValAlaSerGluAla 303
DB 1001 TCTCTATACAGAGTAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1060
OY 304 ValArgAlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
DB 1061 GTTCGTGCTTGTAGAAACTAGTAAATAATACCAAGTATACATAGCCCTGCTCGAA 1120
OY 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTyrPheTyrAspLeuGlyIleLysTyr 343
DB 1121 ACCTTATACCTACTCTCTGAGGTGGAGCATGTGATCTATGATTTGGGCATCAATAT 1180
OY 344 SerPhe-----Th 346
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DB 1181 TCGTTTACAACTGAACTTCGAGATACGGGCACATACGAGATTCTGCTCCGAGCGTTAC 1240
OY 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
DB 1241 ATCAAAACCCACTGTAGAGAAAGCTTTGGCGCTGTCTCTTAA 1283

RESULT 4
US-08-277-540-2
; Sequence 2, Application US/08277540
; Patent No. 5474901
; GENERAL INFORMATION:
; APPLICANT: Drayna, Dennis T., Eaton, Dan L.
; TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/277,540
; FILING DATE: 19-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167727
; FILING DATE: 15-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/959944
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/649591
; FILING DATE: 01-FEB-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 689D1C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; FAX: 415/952-9881
; TELETYPE: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1749 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-277-540-2

Alignment Scores:
Pred. No.: 3,51e-219 Length: 1749
Score: 1832.00 Matches: 357
Percent Similarity: 86.27% Conservative: 1
Best Local Similarity: 86.02% Mismatches: 2
Query Match: 95.87% Indels: 55
DB: 1 Gaps: 2

US-09-980-881A-2 (1-360) x US-08-277-540-2 (1-1749)
OY 1 MetLysLeuGlnSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
DB 41 ATGAACCTTTGACAGCTTCACAGCTTGTACCATTTGCTCTTCTGTCGACAGCATGTC 100
OY 21 PheAlaPheGlnSerGlyGlnValLeuAlaIleuProArgThrSerArgGlnValGln 40
DB 101 TTCGGTTCAGAGTGGCCAAAGTTCAGCTGCTTCTCTAGAACCTCTTAGCCAACTTCAA 160
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QY 41 ValLeuGlnAsnLeuThrThrTyrGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAAATCTTACTACACATATGACATTTGTTCTCGGACGCGGTAACAGCTGAC 220
QY 61 LeuIleValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 221 CTATTTGTGAAGAAAAAACAAGTCATTTTGTAAATCATCTGATGTCGACAAATGTG 280
QY 81 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 100
Db 281 AAGGCCATTAAATGTGACCGGAATTCATGCAAGTCTTGTCTGGCAGACGCTGGAGAT 340
QY 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 341 CTATTATCAACAGCAGATTTCCACAGCAGCAGTACGCCCCGAGCGCTCGCATGCTACTAT 400
QY 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 401 GAACAGATACACACACAAATGAATCTATCTTGATGAATTAATTAACAGAGGACAT 460
QY 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 461 CCGATATATGCTTACAAAAATCCACATTTGATCTCTATTAGAAATGCCACCTTATGTT 520
QY 161 LeuLysValSerGlyLysGlnIleThrAlaLysAsnAlaIleTrpIleAspCysGlyIle 180
Db 521 TTTAAGGTTCTGGAAAAAGAAACAAGCAAAATGCCATATGATGATGACTGTGATATC 580
QY 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis----- 197
Db 581 CATGCCAGAAATGATCTCTCTGCTTCTGCTGTTGTTGATAGCCATATAACTCAA 640
QY 197 ----- 197
Db 641 TTCTATGGATAATAGGCAATATACCAATCTCTGAGCTTGATGTTCTATGTTATG 700
QY 198 -----AsnArgMetTrpArgLys 203
Db 701 CCGGTGTTAATGTGACGCTTATGACTACTCATGAAAAAGATCGAATGTGAGAAAG 760
QY 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheVal 223
Db 761 AACCGTTCTTCTATGCGAAACAATCATCTGCAACAGACCTGAAATAGCAACTTTGCT 820
QY 224 SerLysHisTrpCysGlnGluGluValAlaSerSerSerCysSerGluTrpTyrCysGly 243
Db 821 TCCAAACACTGCTGTGAGAAAGTGCATCCAGTTCTCATGCTCGGAAACCTTACTGTGA 880
QY 244 LeuTyrProGlnSerGluProGluValAlaValAlaSerPheLeuArgArgAsnIle 263
Db 881 CTTTATCTGAGTCAGAACCAAGAGTAGAGAGTGTGCTTCTTGAGAGAAATATC 940
QY 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
Db 941 AACCAAGTTAAACATATACATCAGCATTCATCCACAGCATATATAGTGTTCATAT 1000
QY 284 SerTyrThrArgSerLysSerLysAspHisGlnGluLeuSerLeuValAlaSerGluAla 303
Db 1001 TCTATATACAGAAAGTAAACCAAGACCATGAGAACTGCTCTAGTAGCCAGTGAAGCA 1060
QY 304 ValArgAlaIleAspLysTrpSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
Db 1061 GTTCGTCTATTGAGAAACTAGTAAATAATACAGATATACATGCGCATGCGTCAGAA 1120
QY 324 ThrLeuTyrLeuAlaProGlyLysGlyLysAspTrpIleTyrAspLeuGlyIleLysTyr 343
Db 1121 ACCTTATACAGTACTCTCTGAGGTGGAGCATGATGATATGATTTGGGATCAATAATAT 1180
QY 344 SerPhe-----Thr 346
Db 1181 TCGTTTACAATTGACATTCGAGATAGCGGCACATACGAGATTCTTGCTGCGGAGCGTTAC 1240

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QY 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360
Db 1241 ATCAAAACCCACCTGTAGAGAGCTTTTGCCGCTGTCTTAA 1283

RESULT 5
US-08-430-787A-2
: Sequence 2, Application US/08430787A
: Patent No. 5593674
: GENERAL INFORMATION:
: APPLICANT: Drayna, Dennis T., Eaton, Dan L.
: TITLE OF INVENTION: No. 5593674el Plasma Carboxypeptidase
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/430,787A
: FILING DATE: 27-APR-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/277,540
: FILING DATE: 19-JUL-1994
: APPLICATION NUMBER: 08/167727
: FILING DATE: 15-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/959944
: FILING DATE: 14-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/649591
: FILING DATE: 01-FEB-91
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 68901C1D1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1749 bases
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-430-787A-2

Alignment Scores:
Pred. No.: 3,51e-219 Length: 1749
Score: 1832.00 Matches: 357
Percent Similarity: 86.27% Conservative: 1
Best Local Similarity: 86.02% Mismatches: 2
Query Match: 95.87% Indels: 55
DB: Gaps: 2

US-09-980-881a-2 (1-360) x US-08-430-787A-2 (1-1749)

QY 1 MetLysLeuCysSerLeuAlaValLeuValProIleValLeuPheCysGluGlnHisVal 20
Db 41 ATGAGCTTTGACACCTTGACAGTCTTGATCCCATTTGTTCTTCTGTGAGCAGCATGTC 100
QY 21 PheAlaPheGlnSerGlyGlnValLeuAlaValLeuProArgTrpSerArgGlnValGln 40
Db 101 TTGCGTTTCAGAGTGGCAGCAATTTCTAGCTGCTTCTTCTGAAACCTTAGGCAAGTTCAA 160

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Qy 41 ValLeuGlnAsnLeuThrThrThyGluIleValLeuTrpGlnProValThrAlaAsp 60
Db 161 GTTCTACAGAACTTACTACACATATGATGTTCTCTGCGACCGGTAACTGAC 220
Qy 61 LeuIleValLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 80
Db 221 CTTATTGTGAAGAAAAACAGTCCATTTTGTAAATGCATCTGATGTCAGCAATGTG 280
Qy 81 LysAlaHisLysAsnValSerGlyLeuProCysSerValLeuLeuAlaAspValGluAsp 100
Db 281 AAGGCCATTTAAATGTCAGCGCATTTCCATGCTGCTGCGACGAGCGTGAAGAT 340
Qy 101 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyr 120
Db 341 CTTATTCAACAGCAGATTTCCAGACACAGTCAGCCCCGCGCTCGCATCTGACAT 400
Qy 121 GluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHis 140
Db 401 GACAGTATCCTCAGTAAATGAAATCTTGTGATGAAATTTAACTGAGAGGCAT 460
Qy 141 ProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrVal 160
Db 461 CCTGATATGCTTACAAAATCCACATTTGATCCTCATTTGAGAACTACCCATCTATGT 520
Qy 161 LeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyTle 180
Db 521 TTTAAAGTTTCTGGAAGAAACAAACACCAAAATGCCATATGATGATGCTGGAATC 580
Qy 181 HisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHis 197
Db 581 CATGCCAGAGATGATCTCTCGCTTCTGCTTGTGTTCTATAGGCCATATATCACTCA 640
Qy 197 197
Db 641 TTCTATGGGATAAAGGCAATATACCAATCTCTGAGCTTGTGATTTCTATGTTATG 700
Qy 198 198
Db 701 CCGGCTGCTTATGTGACGCTTATGACTACTCATGAAAGAAATCGAATCTGGAGAAG 760
Qy 204 AsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAspPheVal 223
Db 761 AACGTTCTTCTATGCGAACAATCATTCATTCGGAACAGCCGATAGCAACTTTTGCT 820
Qy 224 SerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGly 243
Db 821 TCCAAACACTGCTGTGAGGAGGTGCATCCAGTTCCTCATGCTCGAAGAACTACTGGA 880
Qy 244 LeuTyrProGluSerGluProGluValLysAlaLysPheLeuArgAsnIle 263
Db 881 CTTTATCTGAGTCAAGAACCAAGAGTGAAGCGTGTGCTGTTCTTGAGAGAAATATC 940
Qy 264 AsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyr 283
Db 941 AACGAGATTAAAGCATCATCATGATCATTCATCCAGCATATAGTGTTCCTAT 1000
Qy 284 SerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAla 303
Db 1001 TCCATATCAGGAAGTAAACCAAGACCATGAGGAAGTCTCTCTAGTACGACGAGCA 1060
Qy 304 ValArgAlaIleAspLysTrpSerLysAsnThrArgTyrThrHisGlyHisGlySerGlu 323
Db 1061 GTTCGTCTCTATGAGAAACTAGTAAATAATACACAGATATACATGGCCATGGCTCAGAA 1120
Qy 324 ThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyr 343
Db 1121 ACCTTATACCTACTCTCTGAGGTGGGAGCATTTGATCTATGATTTGGGCATCAATAT 1180
Qy 344 SerPhe 1180
Db 1181 TCGTTTACAAATTAACACTTCGAGATAGCGGCACATACGATTTCTTGTGCGGAGCGTTAC 1240
Qy 346 rSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 360

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Db 1241 ATCAAAACCCACTGTAGAGAGCTTTTGGCGCTGTCTCTAATA 1283
RESULT 6
US-08-696-139-1
: Sequence 1, Application US/08696139
: Patent No. 5672496
GENERAL INFORMATION:
: APPLICANT: Fayerman, Jeffrey T.
: APPLICANT: Greenen, David P.
: APPLICANT: Hershberger, Charles L.
: APPLICANT: Larson, Jeffrey L.
: APPLICANT: Sterner, Jane L.
: APPLICANT: Zhang, Haichao
: TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
: NUMBER OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Eli Lilly and Company
: STREET: Lilly Corporate Center
: CITY: Indianapolis
: STATE: Indiana
: COUNTRY: United States of America
: ZIP: 46285
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/696,139
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/153,258
: FILING DATE: 16-NOV-1993
ATTORNEY/AGENT INFORMATION:
: NAME: Gaylo, Paul J.
: REGISTRATION NUMBER: 36,808
: REFERENCE/DOCKET NUMBER: X-8681
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (317) 276-0756
: TELEFAX: (317) 276-3861
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1215 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1215
US-08-696-139-1
Alignment Scores:
Pred. No.: 3,22e-70
Score: 640.50
Percent Similarity: 54.29%
Best Local Similarity: 37.67%
Query Match: 35.52%
DB: 1
Gaps: 6
US-09-980-881a-2 (1-360) x US-08-696-139-1 (1-1215)
Qy 23 PheGlnSerGlyGlnValLeuAlaLeuProValGlyThrSerArgGlnValGlnValLeu 42
Db 28 TTTGGAAGGGGAGAGGTTTCCGTTCATGTGAAGATGAATAATGACATCAGCTTACTC 87
Qy 43 GlnAsnLeuThrThrThyGluIleValLeuTrpGlnProValThrAlaLysPheLeu 62
Db 88 CATGACTTGCCAGCAGCAGCAGATTCCTTGTGGAACCAAGATTTGTGTACACCAATTC 147

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Oy	63	VallyslYslYsglVnVlHlSphePheValAsnAlaSerValAspValLysAla	82
Db	148	AAACCTCAGCACTACAGTTGACTTCCTCGTGTGAAGCAAGAAATATTTGGCTGTGAAGAC	207
Oy	83	HlSeuAnValSerGlyIleProCysSerValLeuAlaAspValGluAspLeuIle	102
Db	208	TTTCTGGAGCAGATGAATACATATATAGATGACTCATTAACACCTGATCTGTGCTC	267
Oy	103	GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln	122
Db	268	GAGGCTCAGTTTGACACACAGATC-----CGTACACCTGGACACAGTTATGAGAG	318
Oy	123	TyrHlSerLeuAnGlnIleTyrSerTrpIleGluPheIleThrPheAspCysGlyIleHisAla	142
Db	319	TACAAACAACTGGGAAGACGATCGAGCCGTGGACATACCAAGTACCAAGTAAATCTCAAC	378
Oy	143	MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys	162
Db	379	CTCATCTCTCCACACCCACGACGACACTACTTTTGGAAACAAATATATACCTCTCTCAAG	438
Oy	163	ValSerGlyLysGlnGlnThrAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla	182
Db	439	GTT---GCCAAACCTGGACCAAAATTAAGCCTGCACATTTTATGACATGtGTTTCATCTCC	495
Oy	183	ArgGlnTrpIleSerProAlaPheCysLeuTrpPheIle-----	195
Db	496	AGAGATATGATTTCCATGCATTTTGGCAGGTGTTGTGAGAGAGGCTGTCTCACATAT	555
Oy	195	-----	195
Db	556	GGATATGAGAGCTCACATGACAGAAATCTCTACACAGCTAGACTTTTATGCTTGGCTGTG	615
Oy	196	-----GlyHis-----AsnArgMetTrpArgLysAsnArg	205
Db	616	CTCAATATTTGATGGCTACATCTACCTACCTGGACCAAGACCGAATGGAGAAAGCCGC	675
Oy	206	SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAnSerAsnPheValSerLys	225
Db	676	TCTACCAATGCTGGAACTACTCTCATTTGGCACAGACCCCAACAGAAATTTT--GATGCT	732
Oy	226	HisTrpCysGlnGlnGlyAlaSerSerSerCysSerGlyThrTyrCysGlyLeuTyr	245
Db	733	GGGGGTGGCAAACTGGAGGCTCTACAGACCCCTGGCATGAGACATCTAGTGTGATCTCT	792
Oy	246	ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln	265
Db	793	GCAAGATCTGAAAAAGACCAAGGCCCTCGGTGATTTTATACGCAACACCTCTCCCTCC	852
Oy	266	IleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr	285
Db	853	ATCAAAGCATACCTGACGATCCACTCATATCTACAGATGATATCTCAACCTTATTCAT	912
Oy	286	ThrArgSerLysSerLysAspHisGlnLeuSerLeuValAlaSerGluValAlaValArg	305
Db	913	GATTACAAACATCCCGCAGAACATGCTGAGTTGAATATACCTGGCTAAAGGCTCCGTGA	972
Oy	306	AlaIleAspLysThrSerLysAsnThrArgTyrThrHisGlyHisIleGlySerGluThrLeu	325
Db	973	GAACT---GCTACACTGTATGGCCACCAAGTACATACATGAGGCCGAGACTACCAACATC	1029
Oy	326	TyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLysTyrSerPhe	345
Db	1030	TATCTCTGCTGCTGGGGCTCTGATGACTGGCGCTTAAGACCAAGATCAATATTCCTTC	1089
Oy	346	Thr 346	
Db	1090	ACC 1092	

RESULT 7
 US-08-860-882A-56
 ; Sequence 56 Application US/08860882A
 ; Patent No. 5985281
 ; GENERAL INFORMATION:

```

1  APPLICANT: TAYLORSON, CHRISTOPHER JOHN
2  APPLICANT: EGGLETON, HENDRIKUS JOHANNES
3  APPLICANT: TARRAGONA-FIOL, ANTONIO
4  APPLICANT: RABIN, BRIAN ROBERT
5  APPLICANT: BOYLE, FRANCIS THOMAS
6  APPLICANT: HENNAM, JOHN FREDERICK
7  APPLICANT: BLAKELEY, DAVID CHARLES
8  APPLICANT: MARSHAM, PETER ROBERT
9  APPLICANT: HEATON, DAVID WILLIAM
10 APPLICANT: DAVIES, DAVID HOW
11 TITLE OF INVENTION: CHEMICAL COMPOUNDS
12 NUMBER OF SEQUENCES: 77
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: PILLSBURY, MADISON & SUTRO
15 STREET: 1100 NEW YORK AVENUE, N.W.
16 CITY: WASHINGTON
17 STATE: D.C.
18 COUNTRY: USA
19 ZIP: 20005
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: Floppy Disk
22 COMPUTER: IBM compatible
23 OPERATING SYSTEM: PC-DOS/MS-DOS
24 SOFTWARE: Patent In Release #1.0, Version #1.25
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: US/08/860,882A
27 FILING DATE: JUNE 23, 1997
28 CLASSIFICATION: 424
29 ATTORNEY/AGENT INFORMATION:
30 NAME: DONALD J. BIRD
31 REGISTRATION NUMBER: 25,323
32 REFERENCE/DOCKET NUMBER: 9901/238653
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (202) 861-3027
35 TELEFAX: (202) 822-0944
36 TELEX: 61174627 CUSH
37 INFORMATION FOR SEQ ID NO: 56:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 1263 bases
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43
44 US-08-860-882A-56
45
46 Alignment Scores:
47 Pred. No.: 5,31e-70 Length: 1263
48 Score: 639.00 Matches: 135
49 Percent Similarity: 53.83% Conservative: 69
50 Best Local Similarity: 35.62% Mismatches: 131
51 Query Match: 33.44% Indels: 44
52 DB: 2 Gaps: 7
53
54 US-09-980-881A-2 (1-360) x US-08-860-882A-56 (1-1263)
55
56 6 leuAlaValleuValProIleValleuPheGluGlnHisValPheAla---PheGln 24
57 ||| ||||| ||||| ||| ||| ||||| |||||
58 4 CTCCTGGTCTGGTGAAGTCTGGTCCCTGGCATCTCTGATCATGCTGGTGGACACTTGGAA 63
59
60 25 SerGlyGlnValleuAlaAlaIleuProAlaGlyHisSerAlaGlyGlnValleuGlnAsn 44
61 ::||| ::||| ::||| ::||| ::||| ::||| ::|||
62 64 GCGCGAGAGGTGCCGCTGGTAAAGCTGGAACATGCAAAATGCATTACATTAATACCGGAG 123
63
64 45 leuThrPThrPThrGlyGlnIleValleuThrGlnProValThrAlaAspIleuIleValLys 64
65 ||| ::||| ::||| ::||| ::||| ::||| ::|||
66 124 TTGGCCACACGACGCCACGATTGACTTGGAGGCCAGATTCCTGTCACACAAATCAAACT 183
67
68 65 LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAlaHisLysLeu 84
69 ||| ||| ||| ||| ||| ||| |||
70 DB CACAGTAAAGTGAAGTCTGCCGCTTAAAGCAGAAAGATATGCTCACTGTGGAGAAATGTTCTA 243
71
72 85 AsnValSerGlyIleProGlySerValleuLeuAlaAspValGluAspLeuIleGlnGln 104
73 ::| ::| ::| ::| ::| ::| ::| ::|
74 244 AAGCGAATGAATCAATCAATCAAGATGATGATTAAGCAACCTGAAATTAATGCTGGAGGCT 303
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Db 415 TCTCGCAGTGTATATCGAACAACATTGAGGAGCGGCTATTACCTCGTGAAGTT--- 471
Oy 165 G1YLSGLUGLInThrAlaIysAsnAlaIleTrpIleAspCysGlyIleHisAlaArgIu 184
Db 472 GGCAGAACTGGCAAAATAAGCCCTGATTCATGACTGTGCTTCATGCCAGAGAG 531
Oy 185 TrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 532 TGGATTTCCTCGCATCTTCGCCAGTGTGTGAAGAGAGGCTGTCTACTATGAGCGT 551
Oy 195 ----- 195
Db 592 GAGATCCAGTGCACAGAGCTTCTGCAGAACTTATAGCTTCTGCTGCTGCATCAT 651
Oy 196 -----GlyHis-----AsnArgMetIrpArgIysAsnArgSerPhe 207
Db 652 ATTGATGGCTACATCTTACACCTGGACCAAGAGCGGATTTTGGAGAAAGACTGCTCCAC 711
Oy 208 TyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPheValSerIysHisTrp 227
Db 712 CATACTGATCTAGCTGATGCTGACACAGACCCACAGAAATTTT---GATGCTGTTGG 768
Oy 228 CysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyrProGlu 247
Db 769 TGTGAATTTGGAGCCCTCTGGAACCCCTGTGATGAACCTTACTGTGACCTGCCGACAG 828
Oy 248 SerGluProGluValIysAlaValAlaSerPheLeuArgArgAsnIleAsnGlnIleIys 267
Db 829 TCTGAAAAGAAACCAAGCCCTGGCTGTGATTCATCCGACAAACTGCTTCATCATCAG 888
Oy 268 AlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyrTrpArg 287
Db 889 GCATATCTGACATCATCAGCTGACTGCTCCAAATGATGATCTACCTTACATATGCTTAC 948
Oy 288 SerIysSerIysAspHisIleGluLeuSerLeuValAlaSerGluAlaValAlaGlnIle 307
Db 949 AAACCTGGTGAACAACATCTGATGTAATGCCCTGCTAAACCTACTGTGAAGAAGACTT 1008
Oy 308 AspIysThrSerIysAsnThrArgTyrThrHisGlyHisGlySerGluThrLeuTyrLeu 327
Db 1009 ---GCCCTACCTGACCGGACACCAAGTACATATGCGCCGGAGCTACACATCTATCCT 1065
Oy 328 AlaProGlyIleGlyAspAspTrpIleTyrAspLeuGlyIleIysTyrSerPheThr 346
Db 1066 GCTGCTGGGGGCTCTGACGACTGGCTTATGACCAAGATCATGATTCCTTACC 1122

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RESULT 9
 US-08-860-882A-71
 Sequence 71, Application US/08860882A
 Patent No. 5985281
 GENERAL INFORMATION:
 APPLICANT: TAYLORSON, CHRISTOPHER JOHN
 APPLICANT: EGGLESTE, HENDRIKUS JOHANNES
 APPLICANT: TARRAGONA-FIOL, ANTONIO
 APPLICANT: RABIN, BRIAN ROBERT
 APPLICANT: BOYLE, FRANCIS THOMAS
 APPLICANT: HENNAM, JOHN FREDERICK
 APPLICANT: BLAKELY, DAVID CHARLES
 APPLICANT: MARSHAM, PETER ROBERT
 APPLICANT: HEATON, DAVID WILLIAM
 APPLICANT: DAVIES, DAVID HOW
 TITLE OF INVENTION: CHEMICAL COMPOUNDS
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PILLSBURY, MADISON & SUTRO
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,882A
; FILING DATE: JUNE 23, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DONALD J. BIRD
; REGISTRATION NUMBER: 25,323
; REFERENCE/DOCKET NUMBER: 9901/238653
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3027
; TELEFAX: (202) 822-0944
; TELEX: 6174627 CUSH
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1284 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-860-882A-71
;
; Alignment Scores:
; Pred. No.: 4.75e-69 Length: 1284
; Score: 631.50 Matches: 129
; Percent Similarity: 54.57% Conservative: 68
; Best Local Similarity: 35.73% Mismatches: 121
; Query Match: 33.05% Indels: 43
; DB: Gaps: 6
;
; US-09-980-881A-2 (1-360) x US-08-860-882A-71 (1-1284)
;
Oy 23 PheGlnSerGlyGlnIleuAlaIleuProArgThrSerArgIleValGlnIleu 42
Db 85 TTTGAGGCGAGAGGTTTCCTGTTTACGTTGAAGATGAATAATACATTACATTAATC 144
Oy 43 GlnAsnLeuThrThrThrTyrGluIleValIleuTrpGlnProValThrAlaAspLeuIle 62
Db 145 CGGAGTTGGCCGACGACCCAGATTGACTTCTGGAAGCCAGATTCCTGTCACCAATC 204
Oy 63 ValIleLysIleGlnValHisPhePheValAsnIleSerAspValAsnValIysAla 82
Db 205 AAACCTCACAGTACAGTGTGACTTCCTGTTTAAAGCAGAGATCTCTCATCTGGAGAA 264
Oy 83 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGlnAspLeuIle 102
Db 265 GTTCTAAGCAGATACATACATACATACAGCTACTGATTAAGCAACCTGAGAAATGTG 324
Oy 103 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTrpGluGln 122
Db 325 GAGGCTCAGTTTGTATAGCGGGTT-----CGTGCAACAGGACACAGTTATGAGAG 375
Oy 123 TyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGluArgHisProAsp 142
Db 376 TACACACAGTGGGAAACGATAGAGGCTTGACATCAACAAGTCCCACTGGAATCCAGCC 435
Oy 143 MetLeuThrIysIleHisIleGlySerSerPheGlySerPheGlySerTyrProLeuTyrValLeu 162
Db 436 CTATCTCTCGCAGTGTATTCGGAACCATTTTGAAGGAGCGCTTATTAACCTCTGGAAG 495
Oy 163 ValSerGlyLysGluGlnThrAlaIysAsnAlaIleTrpIleAspCysGlyIleHisAla 182
Db 496 GTT---GGCAACCTGGACAAATAATAGCCCTGCCATTTTCAATGACGTGTTTCCATGCC 552
Oy 183 ArgIleTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
Db 553 AGAGAGTGTATTCCTCTGATTCGCAAGTGTGTTGAAGAGAGGCTGTCTACTATAT 612
Oy 195 ----- 195
Db 613 GCAGCTGAGATCCAGATGACAGAGCTTCTCGACAACTTATAGCTTATGCTGCTG 672
Oy 196 -----GlyHis-----AsnArgMetIrpArgIysAsnArg 205

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Score: 604.00 Matches: 125
 Percent Similarity: 60.14% Conservative: 44
 Best Local Similarity: 44.48% Mismatches: 72
 Query Match: 31.61% Indels: 41
 DB: 5 Gaps: 5

US-09-980-881A-2 (1-360) x PCT-US96-00995-5 (1-922)

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QY 115 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGlnIleTyrSerTrpIleGlu 134
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Db 1 GCAAGTGGACACACTACACCACTACACCACTGGCAACAGCTGAGCGCTGATTCAA 60
QY 135 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 154
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Db 61 CAAGTGGCACTGATATTCACAGACCTGTCTCAGAGCCCTGATGGACACCACTTTGAA 120
QY 155 LysTyrProLeuTyrValIleLeuValSerGlyLysGluGlnTrpAlaLysAsnAlaIle 174
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 121 GGACGTAACATGTAATGCTCCACAGATT--GGTAACCTAGACCGAATTAAGCCCTCATC 177
QY 175 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 194
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 178 TTCATCATGTGTGTCTTCATGCACAGAGACTGATTTCTCTCGATTCTGTCACTGGTTT 237
QY 195 Ile----- 195
    :::
Db 238 GTGAGAGAGCTGCTCGTACCTTATATCAAGATCCACATGAACAGCTTCTAGATGAA 297
QY 196 -----GlyHis----- 197
    :::
Db 298 CTGGAATTCTATGTCTGCTGCTGGTGCACATGTGATGTGCTATGTCTACCTGGACTAG 357
QY 198 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 217
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 358 GACAGATGTGGAGAAACCCGCTACTAGTGGCTGGAGTTCCTGCTGGGTGTGAC 417
QY 218 LeuAsnSerAsnPheValSerLysHisTrpCysGluGlnIleLysSerSerSerCys 237
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 418 CCCACAGAGAAATTTT--AATGCTGGCTGTGTGAAGTGGAGCTTCTCGAGAGCCCTGC 474
QY 238 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 475 TCTGAACCTTACTGTGGACCAAGCCCGAGAGTCTGAAAAGACAAAGGCCCTGGCAGAT 534
QY 258 PheLeuArgArgHisIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 277
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Db 535 TTCATCGCAACAACCTCTCCACCATCAAGCGCTACCTGACATCCACTCATCTACAG 594
QY 278 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 297
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 595 ATGATGCTTACCTTACTCTCTATGATCAAACTGCCCTGAGAACTATGAGGAATTCAT 654
QY 298 LeuValAlaSerGluAlaValArgAlaIleAspLysThrSerLysAsnTrpArgTyrThr 317
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 655 GCCCTGGTGAAGAGCGGCAAGAGAGCTT--GCCACTCTGCATGGCCACCAAGTACACA 711
QY 318 HisGlyHisGlySerGluThrLeuAlaProGlyLysGlyLysAspTrpIleTyr 337
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 712 TATGGCCCAAGAGCTACCAACATCTATCTGCTGCTGGGAGATCTGAGCACTGGTCTAT 771
QY 338 AspLeuGlyLysTyrSerPheThrSerAsnProProValGluLysLeuLeuProLeu 357
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Db 772 GATCAGAGGATCAAAATATTCCTTACCTTGAAGT--CCGGATACAGGCTTCTTGCTT 830
QY 358 Ser 358
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Db 831 TCT 833
  
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RESULT 15
 US-08-696-139-3
 : Sequence 3, Application US/08696139
 : Patent No. 5672496
 : GENERAL INFORMATION:

```

: APPLICANT: Fayerman, Jeffrey T.
: APPLICANT: Greenen, David P.
: APPLICANT: Hershtberger, Charles L.
: APPLICANT: Larson, Jeffrey L.
: APPLICANT: Sterner, Jane L.
: APPLICANT: Zhang, Haichao
: TITLE OF INVENTION: PANCREATIC CARBOXYPEPTIDASE B
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: STREET: Lilly Corporate Center
: CITY: Indianapolis
: STATE: Indiana
: COUNTRY: United States of America
: ZIP: 46285
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/696,139
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/153,258
: FILING DATE: 16-NOV-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Gaylo, Paul J.
: REGISTRATION NUMBER: 36,808
: REFERENCE/DOCKET NUMBER: X-8681
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (317) 276-0756
: TELEFAX: (317) 276-3861
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 921 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..921
: US-08-696-139-3
:
: Alignment Scores:
: Pred. No.: 2,41e-62 Length: 921
: Score: 576.00 Matches: 116
: Percent Similarity: 59.09% Conservative: 40
: Best Local Similarity: 43.94% Mismatches: 68
: Query Match: 30.14% Indels: 40
: DB: 1 Gaps: 5
:
: US-09-980-881A-2 (1-360) x US-08-696-139-3 (1-921)
:
QY 120 TyrGluGlnTyrHisSerLeuAsnGlnIleTyrSerTrpIleGluPheIleThrGluArg 139
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Db 16 TATGAGAGTACACCACTGGCAACGATCGAGGCTTGGACTAGCAAGCTACCACTGAA 75
QY 140 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 159
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 76 AATCCAGACCTCATCTCTCGACAGCATCGGAACATCAATTTTATAGAAACATATATAC 135
QY 160 ValLeuLysValSerGlyLysGluGlnTrpAlaLysAsnAlaIleTrpIleAspCysGly 179
    ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 136 CTCCTCAAGTTT--GGCAAACTGGAGCAACAATAAAGCTTTCATTTTCATGAGCTGTGT 192
QY 180 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 195
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Db 193 TTCATGCGCAAGAAATGATTTCTCCATGCAATTTTGGCAGTGTGTGTGTGAGAGAGCTGTT 252
  
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QY 195 ----- 195
Db 253 CTCACCTATGATATGAGATCAGATCAGAAATTCCTCAACAAGCTAGACTTTATATGC 312
QY 196 ----- -GLYHis----- -AsnArgMetTrpArg 202
Db 313 TTGCCCTGTGCTCATATTTGATGTGGCTTACATCTACACCTGCACCAAGAACGAATGTGAGA 372
QY 203 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnSerAsnPhe 222
Db 373 AAGACCCGGCTCTACCAATGCTGGAATCTGACATCTGGCAGACAGACCCCAACAGAAATTTT 432
QY 223 ValSerLysHisTrpCysGluGlyAlaSerSerSerCysSerGluThrTyrCys 242
Db 433 --GATGCTGGGTGGTGCACAACTCCCGAGAACAAATGCTGATGACCCCTGCGATGAGACTTACTGT 489
QY 243 GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgAsn 262
Db 490 GGATCTGCTGCAGAGTCTGAAAAAGAGACCAGGCCCTGGCTGATTTTATACGCAACAC 549
QY 263 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 282
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QY 323 GluThrLeuTyrLeuAlaProGlyGlyGlyAspAspTrpIleTyrAspLeuGlyIleLys 342
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Job time : 60.0847 secs

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GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 03:14:57 ; Search time 32.9407 Seconds
(without alignments)
3146.770 Million cell updates/sec

Title: US-09-980-881A-3

Perfect score: 1798
Sequence: 1 FQSGQVLAALPRTSRQVQL.....IKYSFTSNPVEKLLPLSLK 338

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LIST=45 -DOCALLIGN=200 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MUTLEN=0 -MAXLEN=2000000000
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-YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXt=7

Database :

1: Issued_Patents.NA:*
2: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1749.5	97.3	1625	4	US-09-813-133A-1 >FD
2	1732	96.3	1749	2	US-08-866-057-1
3	1732	96.3	1749	1	US-07-649-591B-2
4	1732	96.3	1749	1	US-08-277-540-2
5	1732	96.3	1749	1	US-08-430-787A-7
6	646.5	35.5	1215	1	US-08-696-139-1
7	637.5	35.5	1263	2	US-08-860-882A-56
8	637.5	35.5	1263	4	US-09-011-769A-38
9	637.5	35.5	1284	2	US-08-860-882A-71
10	637.5	35.5	1284	4	US-09-011-769A-55
11	619.5	34.5	1311	4	US-09-675-305-9
12	619.5	34.5	2154	4	US-09-171-945-124

13	610	33.9	927	2	US-08-782-760-5	Sequence 5, Appli
14	610	33.9	927	1	PCR-US96-00995-5	Sequence 5, Appli
15	582	32.4	921	1	US-08-696-139-3	Sequence 3, Appli
16	571.5	31.8	2128	4	US-09-675-305-13	Sequence 13, Appli
17	567	31.5	999	2	US-08-860-882A-67	Sequence 67, Appli
18	567	31.5	999	4	US-09-011-769A-50	Sequence 50, Appli
19	567	31.5	1053	2	US-08-860-882A-64	Sequence 64, Appli
20	567	31.5	1053	4	US-09-011-769A-46	Sequence 46, Appli
21	560	31.1	1059	2	US-08-860-882A-74	Sequence 74, Appli
22	560	31.1	1059	4	US-09-011-769A-59	Sequence 59, Appli
23	559	31.1	1059	2	US-08-860-882A-77	Sequence 77, Appli
24	559	31.1	1059	4	US-09-011-769A-63	Sequence 63, Appli
25	554	30.8	1200	4	US-09-710-099-7	Sequence 7, Appli
26	549	30.5	1870	4	US-09-171-945-112	Sequence 112, App
27	534.5	29.7	1050	4	US-09-675-305-11	Sequence 11, Appli
28	527.5	29.3	1311	4	US-09-710-099-5	Sequence 5, Appli
29	516.5	28.7	1251	3	US-08-640-906-3	Sequence 3, Appli
30	516.5	28.7	1251	4	US-09-395-936-3	Sequence 3, Appli
31	491.5	27.3	1257	3	US-08-640-906-1	Sequence 1, Appli
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35	465.5	25.9	2247	4	US-09-710-099-15	Sequence 15, Appli
36	441	24.5	1056	4	US-09-710-099-9	Sequence 9, Appli
37	441	24.5	1056	4	US-09-710-099-1	Sequence 1, Appli
38	365	20.3	55827	4	US-09-813-133A-3	Sequence 3, Appli
39	288.5	16.0	741	4	US-09-675-305-5	Sequence 5, Appli
40	210.5	11.7	591	4	US-09-331-709-2	Sequence 2, Appli
41	198.5	11.0	629	4	US-09-280-116-228	Sequence 228, App
42	169.5	9.4	515	4	US-08-998-416-125	Sequence 125, App
43	133.5	7.4	673	4	US-09-280-116-93	Sequence 93, Appli
44	116.5	6.5	2504	1	US-08-484-105-15	Sequence 15, Appli
45	116.5	6.5	2504	1	US-08-484-106-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
US-09-813-133A-1
Sequence 1, Application US/09813133A
Patent No. 6455294
GENERAL INFORMATION:
APPLICANT: CAN, weiniu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
FILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1625
TYPE: DNA
ORGANISM: Human
US-09-813-133A-1
Alignment Scores:
Pred. No.: 8.75e-210
Score: 1749.50
Percent Similarity: 94.38%
Best Local Similarity: 94.38%
Query Match: 97.30%
DB: 4
Gaps: 1
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DB 83 TTTCACAGTGGCCAGCTTACCTGCTCTTCCCTAGACCTTAGGCACTTCAAGTTCTTA 142
QY 21 GlnAsnLeuThrThrTyrgIuValIleuTrpGlnProValThrAlaAspLeuIle 40
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QY 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuValAspValGluAspLeuIle 80
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QY 141 ValSerGlyLysGlnGlnTrpAlaLysAsnAlaIleTrpIleAspCysGlyIleHisAla 160
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QY 161 ArgGluTrpIleSerProAlaPheCysLeuTrpPheIleGlyHisAsnArgMetTrpArg 180
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QY 181 LysAsnArgSerPheTyrLysAsnAsnHisCysIleGlyThrAspLeuAsnArgAsn 200
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QY 201 AlaSerLysHisTrpCysGlnGlnGluLysAlaSerSerSerSerGlnTrpTyrCys 220
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QY 221 GlyLeuTyrProGluSerGlnProGluValLysAlaValAlaSerPheLeuArgArgAsn 240
Db 743 GGACTTTATCTGAGTCAGACAAACAGAAAGGAGGAGTGTCTTGGAAAGAAAT 802
QY 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro 260
Db 803 ATCAACCAAGATTAAACATATACATGATCATCTATCTCCAGCATATAGTGTCCA 862
QY 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValAlaSerGlu 280
Db 863 TATTCCTATACAGCAAGTAAGAAAGCAAGCATGAGGAAGCTGTCTTACTAGCCAGTGA 922
QY 281 AlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer 300
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QY 301 GluThrLeuTyrLeuAlaProGlyGlyAspAspTrpIleTyrAspLeuLysIleLys 320
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QY 321 TyrSerPhe----- 323
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RESULT 2
US-08-869-057-1
: Sequence 1, Application US/08869057
: Patent No. 5985562
: GENERAL INFORMATION:
: APPLICANT: Morser, Michael J
: APPLICANT: Nagashima, Mariko

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```

: TITLE OF INVENTION: Method of Detecting Thrombotic Disease
: TITLE OF INVENTION: Risk
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Berlex Biosciences Legal Department
: STREET: 15049 San Pablo Avenue
: CITY: Richmond
: STATE: California
: COUNTRY: USA
: ZIP: 94804-0099
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/869,057
: FILING DATE: 03-JUN-1997
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Washlien, Wendy L.
: REGISTRATION NUMBER: 36,301
: REFERENCE/DOCKET NUMBER: 51509AUSM1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 510-262-5411
: TELEFAX: 510-262-7095
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1272 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: PUBLICATION INFORMATION:
: AUTHORS: Eaton, Dan L.
: AUTHORS: Malloy, Beth E.
: AUTHORS: Tsai, Siao P
: AUTHORS: Henzel, William
: AUTHORS: Drayna, Dennis
: TITLE: Isolation, Molecular Cloning, and Partial
: TITLE: Characterization of a No. 5985562el Carboxypeptidase B
: JOURNAL: J. Biol. Chem.
: VOLUME: 266
: ISSUE: 32
: PAGES: 21833-21838
: DATE: No. 5985562 15-1991
: US-08-869-057-1
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: Query Match: 96.33% Indels: 55
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: QY 21 GlnAsnLeuThrThrThrTyrGlnIleValLeuTrpGlnProValThrAlaAspLeuIle 40
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: QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
: Db 187 GTGAAGAAAACAAAGTCCATTTTGTGTAATGATCATCTGATGTGCGCAATGTGTAAGGCC 246
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QY 304 TyrlLeuAlaProGlyLysGlyAspAspTrpIleTyAspLeuGlyIleLysTySerPhe 323
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QY 324 324
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QY 326 nProProValGluLysLeuLeuProLeuSerLeuLys 338
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RESULT 3
US-07-649-591B-2
: Sequence 2, Application US/07649591B
: Patent No. 5206161
: GENERAL INFORMATION:
: APPLICANT: Dennis Drayna and Daniel Eaton
: TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase

```

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: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: palin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/649,591B
: FILING DATE: 19910201
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 689
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/266-1896
: TELEFAX: 415/952-9881
: TELEX: 910/371-7168
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1749 bases
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: hybridization probe
: LOCATION: 133 to 178
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: FEATURE:
: NAME/KEY: potential clip site
: LOCATION: 380 to 382
: IDENTIFICATION METHOD:
: OTHER INFORMATION:
: NAME/KEY: signal sequence
: LOCATION: 41 to 106
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: OTHER INFORMATION:
: US-07-649-591B-2
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: Pred. No.: 1,57e-207 Length: 1749
: Score: 1732.00 Matches: 338
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: QY 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValLeu 20
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: QY 21 GlnAsnLeuThrThrTyrgInIleValLeuTrpGlnProValThrAlaAspLeuIle 40
: Db 167 CAGATCTTACTACAAACATATGAGATGTCTCTGCGAGCGGTAACAGCTGACCTTAT 226
: QY 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerSpsValAspAsnValLysAla 60
: Db 227 GTGAGAGAAAGAACAGTCAATTTTGTAAATGCATGTGATGCAATGTGAAAGCC 286

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QY 161 ArgIuTPRIleSerProAlaPheCysLeuTPRIheIle----- 173
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QY 173 ----- 173
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QY 174 -----GlyHis-----AsnArgMetIleTPRIgIlyAsnArg 183
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QY 184 SerPheTyrIlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheIleSerIys 203
Db 676 TCTACCAATGCTGGAACTACTCTCATTTGGCACAGACCCCAAGAAATTTT---GATGCT 732
QY 204 HisTPCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 733 GGGGTGGTGCACAACTGGAGCCCTCTACAGACCCCTGGAGATGAGACATTCATGTGATCTCT 792
QY 224 ProGluSerIleProGluValIlyAlaValAlaIleSerPheLeuArgAsnIleAsnIle 243
Db 793 GCAAGATGCTAAAAGAGACCAAGGCCCGCTGGATTTTATTCGCAACACCTCTCCCTCC 852
QY 244 IleIysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 853 ATCAAGACATACCTGAGACATCCACTATCTACAGATGATATCTCACTACCTTATTTCTAT 912
QY 264 ThrArgSerIlySerIysAspHisGluGluLeuSerLeuValAlaSerIleuAlaValArg 283
Db 913 GATTACAAATCCCCCGAGACAAATGCTGAGTTGAATTAACCTGCTAAGGCTCCGTGA 972
QY 284 AlaIleGluYthrSerIysAsnThrArgTyrThHisGlyHisGlySerIleuThrLeu 303
Db 973 GAACTT---GCTACACTGTATGGCACCAAGTACATACGGCCCGAGACTCTCAACAACTC 1029
QY 304 TyrIleuAlaProGluGlyIlyAspAspTPRIleTyrAspLeuGlyIleIlystYrSerPhe 323
Db 1030 TATCTCTGCTGCTGGGGGCTGTGATGACTGGGCTTATGACCAAGATCAATATTTCTTTC 1088
QY 324 Thr 324
Db 1090 ACC 1092

RESULT 7
US-08-860-882A-56
: Sequence 56, Application US/08860882A
: Patent No. 5985281
: GENERAL INFORMATION:
: APPLICANT: TAYLORSON, CHRISTOPHER JOHN
: APPLICANT: EGGLETE, HENRIRUS JOHANNES
: APPLICANT: TARRAGONA-FIOL, ANTONIO
: APPLICANT: RABIN, BRIAN ROBERT
: APPLICANT: BOYLE, FRANCIS THOMAS
: APPLICANT: HENNAM, JOHN FREDERICK
: APPLICANT: BLAKELY, DAVID CHARLES
: APPLICANT: MARSHAM, PETER ROBERT
: APPLICANT: HEATON, DAVID WILLIAM
: APPLICANT: DAVIES, DAVID HOW
: TITLE OF INVENTION: CHEMICAL COMPOUNDS
: NUMBER OF SEQUENCES: 77
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PILLSBURY, MADISON & SUTRO
: STREET: 1100 NEW YORK AVENUE, N.W.
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:

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[illegible]

Db 763 GGTGGTGTGAAATTTGAGCCCTCTCGAAACCCCTGTGATGAACCTACTGTGAGCCTGCC 822
Oy 224 ProgluSerGluProgluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 823 GCAGAGTCTGAAAAGAAACCAAGCCCTGGCTGATTTATCGGCAACAACCTCTTCC 882
Oy 244 IleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 883 ATCAAGCATATCTGCATATCCACTGCTACTCCCAATGATGATCTACCTTATCATAT 942
Oy 264 ThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 943 GCTTACAACTCGGTGAGAACATGCTGAGTTGAATGCCCTGGCTTAAGCTACTGTGA 1002
Oy 284 AlaIleGluLysThrSerLysAsnThrArgTyrThrHisGluHisGlySerGluThrLeu 303
Db 1003 GAACCT---GCCCATCTGCAGCGCCACCAAGTACATATATGCCCCGGAGCTACAAATC 1059
Oy 304 TyrLeuAlaProGluLysAlaAspArgTyrIleTyrAspLeuGluIleLysTyrSerPhe 323
Db 1060 TATCCGTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGAAATCATATCTCTTC 1119
Oy 324 Thr 324
Db 1120 ACC 1122
RESULT 9
US-08-860-882A-71
Sequence 71, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGELTE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAM, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID WILLIAM
APPLICANT: DAVIES, DAVID HOW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-860-882A-71
Alignment Scores:
Pred. No.: 3,85e-70 Length: 1284
Score: 637.50 Matches: 130
Percent Similarity: 54.85% Conservative: 68
Best Local Similarity: 36.01% Mismatches: 120
Query Match: 35.46% Indels: 43
DB: 2 Gaps: 6
US-09-980-881a-3 (1-338) x US-08-860-882A-71 (1-1284)
Oy 1 PheGlnSerGluGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 85 TTTGAAGCGGAGAGAGGTGTTCCGTGTTAAAGTTGAAGATGAATAATCAATTACATTAATC 144
Oy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTyrGlnProValThrAlaAspLeuIle 40
Db 145 CGCGAGTTGGCCGACGACGACGACGATTTGACTTCTGGAAGCAGATTTCTGTACACAAATC 204
Oy 41 ValLysLysGlnValHisPhePheValAsnAlaSerAspValAlaAspAsnValLysAla 60
Db 205 AAACCTCACAGTACAGTTGACTTCCGTGTTAAAGCAGAGATCTCTCAGCTGGAGAAAT 264
Oy 61 HisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAspLeuIle 80
Db 265 GTTCTTAAGCAGATGACATACATACAAAGCTCTGATTAAGCAACCTGGAATATGTTGGT 324
Oy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 325 GAGGCTCAGTTGATGATGACCGGGTT-----CGTCAACAGACACAGATTAAGAGAG 375
Oy 101 TyrHisSerLeuAsnGlnIleTyrSerTyrIleGluPheIleThrGluArgHisProAsp 120
Db 376 TACAACAAGTGGGAAACGATAGAGGCTTGACTGACCAACAGTCCCTGAGATCCAGCC 435
Oy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 436 CTGATCTCTGCGAGTGTATTCGGAACACATTTGAGGAGCGCCCTTTTAACTCCGTGAAG 495
Oy 141 ValSerGlyLysGluGlnThrAlaLysAsnAlaIleTyrIleAspCysGlyIleHisAla 160
Db 496 GTT---GGCAACCTGACGACAAATAAGCCGATTTTCATGTGACTGTGGTTCCATGCC 552
Oy 161 ArgGluTyrIleSerProAlaPheCysLeuTyrPheIle----- 173
Db 553 AGAGAGTGAATTTCTCTGATCTGCGAGTGGTTGTAGAGAGCTGTTCCTACTTAT 612
Oy 173 ----- 173
Db 613 GCAGGTGAGATCCAGTAGACAGAGCTTCTGACAGATTAGCTTTATGTCGCTGG 672
Oy 174 -----GlyHis-----AsnArgMetTrpArgLysAsnArg 183
Db 673 CTCATATTTGATGCTACATCTACACCTGAGCCAGACGCGGATTTTGGAGAAAGACTCCG 732
Oy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 733 TCCACCATATCTGATCTGACTGATTCGACAGACCCCAAGCAAAATTTT---GATGCT 789
Oy 204 HisTrpCysGluGluLysAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 790 GGTGGTGAATTTGGAGGCTCTCGAAACCCCTGTGATGATTAACCTTACGTGAGCCTGCC 849
Oy 224 ProgluSerGluProgluVallyAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 850 GCAGAGTCTGAAAAGAGACCAAGCCCTGGCTGATTTCTCCGCAACAACAACCTCTTCC 909
Oy 244 IleValAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPheProTyrSerTyr 263
Db 910 ATCAAGCATATCTGCATATCCACTGCTACTCCCAATGATGATCTACCTTATCATAT 969
Oy 264 ThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGluAlaValArg 283

Db 970 GCTTACAAACGTCGTGAGAACATGCTGATGTAATGCCCTGCTAAAGCTACTGTGAAA 1029
Qy 284 AAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisIleSerGluThrLeu 303
Db 1030 GAACCTT--GCCTCAGTCGACGCGCACCAAGTACACATATGACCCGCGAGCTACAAACAC 1086
Qy 304 TTTLeuAlaProGlyGlyLysAspPrtPileTyrAspLeuGlyIleLysTyrSerPhe 323
Db 1087 TTTCTGCGCTGGGGGCTCTGACGACCTGCTATGACCAAGAAATCATTTCTTTC 1146
Qy 324 Thr 324
Db 1147 ACC 1149
RESULT 10
US-09-011-769A-55
Sequence 55, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
BLAXEY, David C.
DAVIES, David H.
HENNAM, John F.
HENNEQUIN, Laurent F.A.
MARSHAM, Peter R.
DOMELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 1284 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1272
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 352..1272
SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-011-769A-55
Alignment Scores: 3.85e-70 Length: 1284
Pred. No.: 637.50 Matches: 130

Percent Similarity: 54.85% Conservatve: 68
Best Local Similarity: 36.01% Mismatches: 120
Query Match: 35.46% Indels: 43
DB: 4 Gaps: 6
US-09-980-881A-3 (1-338) x US-09-011-769A-55 (1-1284)
Qy 1 PheGlnSerGlyGlnValLeuAlaIleuProArgThrSerArgGlnValGlnValLeu 20
Db 85 TTTGAAGGCGAAGAGTGTTCCTGTTAACGTTGAAGATGAATAATCATTATTAATATC 144
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuThrGlnProValThrAlaAspLeu 40
Db 145 CGGAGATTGCGCCAGCAGCAGCCAGATTGACTTCTGGAAGCCAGATTCTGTACACAAATC 204
Qy 41 ValLysLysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnValLysAla 60
Db 205 AAACCTCACAGTACAGTGTACTCGTGTAAAGCAGAGATACGTGCTGAGAGAT 264
Qy 61 HisLeuAsnValSerGlyTyrLeuProCysSerValLeuLeuAlaAspValGluAspLeu 80
Db 265 GTTCTTAAGCAGATGACTACATACAAAGTACTGATATAGCAACCTGGAATGTGTG 324
Qy 81 GlnGlnGlnIleSerAsnAspThrValSerProArgAlaSerAlaSerTyrTyrGluGln 100
Db 325 GAGGCTCAGTTGATAGCCGGGT-----CGTCAACGAGACAGATTATGAGAG 375
Qy 101 TyrHisSerLeuAsnGluIleTyrSerTyrPheGluPheIleThrGluArgHisProAsp 120
Db 376 TACAACAACTGGGAAACGATAGAGCTTGACTACAAAGTGGCCACTGAGATCCAGCC 435
Qy 121 MetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyrValLeuLys 140
Db 436 CTCATCTCTCCGAGGTATATGGAACACATTTGAGGAGCGCGATATTAACCTCTGAG 495
Qy 141 ValSerGlyLysGlnGlnThrAlaLysAsnAlaIleTyrPheAspCysGlyIleHisAla 160
Db 496 GTT---GGCAAGCTGAGCAAAATAGCCCTGATTTTCATGAGCTGAGTTCCATGCC 552
Qy 161 ArgGluTyrPheSerProAlaPheCysLeuTyrPheIle----- 173
Db 553 AGAGAGTGGATTCTTCGCAATTTGCGCAGTGTGTTGTAAGAGAGCTGTTCCTACT 612
Qy 173 ----- 173
Db 613 GCAGCTGACATCCAGTGCAGAGAGCTTCGACAGATTAGATTTTATGCTGCTGCG 672
Qy 174 -----GlyHis-----AsnArgMetTyrArgLysAsnArg 183
Db 673 CTCATATTGATGGCTACATCTACACCTGAGCAAGAGCGGATTTTGAGAAAGACTGCG 732
Qy 184 SerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPheAlaSerLys 203
Db 733 TCCACCACATGATGATCTAGCTGCAATTGGCAGACAGCCCAACAGAAATTTT---GATCGT 789
Qy 204 HisTyrCysGluGluGlyAlaSerSerSerCysSerGluThrTyrCysGlyLeuTyr 223
Db 790 GGTGTGTGTAATGGAGAGCCCTCGAAACCCCTGTGATGAATCTAGTGGAGCTGCC 849
Qy 224 ProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsnIleAsnGln 243
Db 850 GCAGAGTCTGAAAGCAGACCAAGCCCTGCTGATTTTCATCCGCAACAACTCTCTCC 909
Qy 244 IleLysAlaTyrIleSerMetHisSerIleSerGlnHisIleValPheProTyrSerTyr 263
Db 910 ATCAAGCATATCTACATCCACTGCTACTCCCAAAATGATGATCTTACCTTACTCATAT 969
Qy 264 ThrArgSerLysSerLysAspHisGlnGluLeuSerLeuValAlaSerGluAlaValArg 283
Db 970 GCTTACAAACGTCGTGAGAACATGCTGATGTAATGCCCTGCTAAAGCTACTGTGAAA 1029
Qy 284 AAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisIleSerGluThrLeu 303

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Db 1030 GAACCT---GCCCTACCTGACGCGACCAAGTACACATATGCCCCGGAGCTACCAACATC 1086
Qy 304 TyrLeuAlaProGluGlyGlyAspAspTrpIleTyrAspLeuGlyIleTyrSerPhe 323
Db 1087 TATCCTGCTGCTGGGGGCTCTGACGACTGGGCTTATGACCAAGGAATCATCTTCTTC 1146
Qy 324 Thr 324
Db 1147 ACC 1149

RESULT 11
US-09-675-305-9
: Sequence 9, Application US/09675305
: Patent No. 6441153
: GENERAL INFORMATION:
: APPLICANT: Donoho, Gregory
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Neuhls, Michael
: APPLICANT: Friedlich, Glenn
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6441153el Human Carboxypeptidases and
: TITLE OF INVENTION: Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0047-USA
: CURRENT APPLICATION NUMBER: US/09/675,305
: PRIOR FILING DATE: 2000-09-29
: PRIOR APPLICATION NUMBER: US 60/156,685
: NUMBER OF SEQ ID NOS: 13
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 1311
: TYPE: DNA
: ORGANISM: homo sapiens
US-09-675-305-9

Alignment Scores:
Pred. No.: 7.3e-68 Length: 1311
Score: 619.50 Matches: 136
Percent Similarity: 51.15% Conservative: 64
Best Local Similarity: 34.78% Mismatches: 127
Query Match: 34.45% Indels: 64
Gaps: 8

US-09-980-881a-3 (1-338) x US-09-675-305-9 (1-1311)
Qy 1 PheGlnSerGlyGlnValLeuAlaLeuProArgThrSerArgGlnValGlnValLeu 20
Db 109 TATGCTGTGATTAAGATTATTTCCCAAAACAGAGAGAGAGCATATGCGACTG 168
Qy 21 GlnAsnLeuThrThrThrTyrGluIleValLeuTrpGlnProValThrAlaSerIle 40
Db 169 AAGAAAATATCTATCAACTTAAGGTGACCTGGCCACCCGACGAGATGTCCTATGTA 228
Qy 41 ValLys-----LysLysGlnValHisPhePheValAsnAlaSerAspValAspAsnVal 58
Db 229 TCAGAGCGAAGACGATTCAGATGTCATATCCCAAAATAGTTCGCGAGCC-----CTG 282
Qy 59 LysAlaHisLeuAsnValSerGlyIleProCysSerValLeuLeuAlaAspValGluAsp 78
Db 283 TTAGCTTCTTACAGAGAGCCAAACATCCAGTCAAGGTCCTCATAGAGATCTTCAGAA 342
Qy 79 LeuIleGlnGlnIleSerAsnAspThrValSerProArgAlaSerIleSer----- 96
Db 343 ACACGTGGAGAAAGGAGAGCGCTTGACACACAGAGAAACCGAAGATCCCTCTCTGGATAT 402
Qy 97 TyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGluPheIleThrGlu 116
Db 403 AATATGAGATTATACACCCCTTAGAGAAATTCAAATATGATGATCATCTGATATAA 462
Qy 117 ArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProIleu 136
Db 463 ACTCACTGAGGCTCATTCACATGTTCTATTGGAAGATCATATAGAGAGATCTCTT 522

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Qy 137 TyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCys 156
Db 523 TTATATTTTAAACCTG---GGCAGAGATTCACAGACTCAACAAAGAGCTGTTGATAGACTCT 579
Qy 157 GlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 580 GGTATTCATGCAAGAGAAATGATGTGCTCCTGCTTTTGTACGTGTTGTAAAGAGACT 639
Qy 173 ----- 173
Db 640 CTTTACATATATAGAGAGTACCCAGCCATGAGAAAATGTGAATCATATATTTCTAT 699
Qy 174 -----GlyHisAsnArgMetTrp 179
Db 700 ATCATGCCGTGTGTTTACCTGCATGATGCATTTAGTTGAGCCATATGATGATTTTGG 759
Qy 180 ArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsn 199
Db 760 AAAAAACAAAGGTCAAGAGAACTCAAGGTTTCGCTGCCGCGAGTGATGCCAATAGAAAC 819
Qy 200 PheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCysSerGluThrTyr 219
Db 820 TCGAAAGTGAAG---TGCGTGATGAGAGAGCTTCATGCACCCCTGTATATACACATAC 876
Qy 220 CysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArg 239
Db 877 TGTGGCCCTTTCCAGAACTGACCGGAGAGTGAAGGCTGTAGCTTCCCTTCGAAAA 936
Qy 240 AsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhe 259
Db 937 CACAGAAACACATATGAGGCTTATCTCTCTTCATGATGCTCAGATGCTAGTACTGAT 996
Qy 260 ProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerIleValAlaSer 279
Db 997 CCCATCTTACAAATATGACCAACATTCACATTTTAGATGCTGGAATCTGCAGCTTAT 1056
Qy 280 GluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlnHisGly 299
Db 1057 AAGCTGTAATGACCTTAGTCAGTA---TACGGGTCAGATACAGATATGACACAGCC 1113
Qy 300 SerGluThrLeuTyrIleuAlaProGluGlyGlyAspAspTrpIleTyrAspLeuGlyIle 319
Db 1114 TCCACAACTGTATGTAGTGTCTGTGTACTCATGATGATGGGCTACAAAAATGAGATA 1173
Qy 320 LysTyrSerPhe----- 323
Db 1174 CCTATGACATTTGCTTTCGAACTACGTGACACTGATATTTTGATTTTACTCCACAG 1233
Qy 324 ---ThrSerAsnProProValGluLysLeu 332
Db 1234 ATGCTCATCAACCCACCTGTACAGAACTA 1264

RESULT 12
US-09-171-945-124
: Sequence 124, Application US/09171945
: Patent No. 6272599
: GENERAL INFORMATION:
: APPLICANT: Emery, Stephen
: APPLICANT: Copley, Clive Graham
: APPLICANT: Edge, Michael Derek
: TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
: TITLE OF INVENTION: Antibody, and Their Therapeutic Use in an Adept System
: FILE REFERENCE: Monoclonal Antibody to CEA
: CURRENT APPLICATION NUMBER: US/09/171,945
: PRIOR FILING DATE: 1998-10-29
: PRIOR APPLICATION NUMBER: GB9703103.3
: PRIOR FILING DATE: 1997-02-14
: PRIOR APPLICATION NUMBER: GB9609405.7
: PRIOR FILING DATE: 1996-05-04
: PRIOR APPLICATION NUMBER: PCT/GB97/01165
: PRIOR FILING DATE: 1997-04-29
: NUMBER OF SEQ ID NOS: 131

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Db      829  GCAAGCTGTAAAGGAGGACCAAGGCCCGTGGCTGATTTTCATCCGACCAAACTCTCTCC 888
QY      244  ILeYsAlaTyrlleSerNethHisSerTYrSerGlnHisIleValaPheProTyrSerTyr 263
          |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      889  ATCAAGCAATATCTGCACAAATCCACTGCTACTCCCAATATGATATCTACCTTACCATAT 948
QY      264  ThrArgSerIysSerIysAspHisGluGluIleuSerLeuValAlaSerGlnAlaValArg 283
Db      949  GCTTACAACACTCGGTGGAACAAATGCTGTGATGTAATGCCCTGCGTAAAGCTACTGTGAAA 1008
QY      284  AlaIleGluIysThrSerIysAsnThrArgTYrThrHisGlyHisGlySerGlnThrIleu 303
          :::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db      1009  GAACCT---GCGTCACGCGACGCGCACCACAGTACACATATGCGCCGGAGCTACAAACATC 1065
QY      304  TyrlleuAlaProGlyGlyGlyAspAspTPrIleTYrAspLeuGlyIleIysTYrSerPhe 323
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Db      1066  TATCTCTCTGCTGCGACTTCTAAAGACTGGGCTTATGACCAAGAAAGATATATCTTC 1125
QY      324  Thr 324
          |||
Db      1126  ACC 1128
RESULT 13
US-08-782-760-5
Sequence 5, Application US/08782760
Patent No. 5948668
GENERAL INFORMATION:
APPLICANT: Hartman, Jacob
APPLICANT: Fulga, Netta
APPLICANT: Mendelovitch, Simona
APPLICANT: Corecki, Marian
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
NUMBER OF SEQUENCES: 8
CARBOXYPEPTIDASE B
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,760
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,233
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0336/43847
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ. ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..927
US-08-782-760-5

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Alignment Scores:

Pred. No.:	6,37e-67	Length:	927
Score:	610.00	Matches:	126
Percent Similarity:	60.50%	Conservative:	44
Best Local Similarity:	44.84%	Mismatches:	71
Query Match:	33.93%	Indels:	41
DB:	2	Gaps:	5

US-09-980-881A-3 (1-338) x US-08-782-760-5 (1-927)

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QY 93 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 112
DB 1 GCAAGTGGACACAGCTACCAAGTACAACTGGAAACGATGAGCGCTGATTCAA 60
QY 113 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerPheGlu 132
DB 61 CAAGTTGCCACTGATATATCCCTTGTCTCAGAGCGTCAATGGACACATTGAA 120
QY 133 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 152
DB 121 GGACGTAACTGATATGCTCTCAAGATT---GGTAAACTAGACCGAATAAGCCTGCCATC 177
QY 153 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 172
DB 178 TTCATCGATTGTGTTCCATGTCAGAGAGTGGATTTCCTCGCATTCCTGAGTGTGTTT 237
QY 173 Ile----- 173
DB 238 GTGAGAGAGGCTGCTCCGTACCTATATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297
QY 174 -----GlyHis----- 175
DB 298 CTGATTTCTATGTTCTGCCGTGGTCAACATTGATGCTATGTCTACACCTGGACTAAG 357
QY 176 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 195
DB 358 GACAGATGCTGAGAAAACCCGCTCTACTATGAGTGGAGATTCCCTGGCTGTAGAC 417
QY 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluValAlaSerSerSerCys 215
DB 418 CCCAAGAGGAATTTT---ATGCTGCTGCTGTGGAGTCTTCTGGAGTCCCTGC 474
QY 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaLysSer 235
DB 475 TCTGAACCTTACTGTGTGACAGCCAGAGTCTGAAAAGAGCAAGGCCCTGGAGAT 534
QY 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrTrpIleSerMetHisSerTyrSerGln 255
DB 535 TTCATCCCGCAACACTCTCCACCATCAAGGCTTACTGACCATCCATCATCTACACAG 594
QY 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275
DB 595 ATGATGCTCTTACCTTACTTACTGTACTGACTACAACTGCTGAGAACATGAGGAATTTGAT 654
QY 276 LeuValAlaSerGluValAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295
DB 655 GCCCTGTGTAAGGTGCGGCAAGAGCTT---GCCACTCTGATGGCACCAGTACACAG 711
QY 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyLysGlyLysAspTrpIleTyr 315
DB 712 TTATGCCCGAGAGCTACCAACATCTTCTGCTGCTGAGGAGATCTGACGACTGCTTAT 771
QY 316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuProLeu 335
DB 772 GATCAGGAAATCAATATTCCTTACCTTGAAGT---CCGGGATACAGGCTTCTTGAGCTT 830
QY 336 Ser 336
DB 831 TCT 833

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RESULT 14
PCT-US96-00995-5

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; Sequence 5, Application PC/TUS9600995
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
; TITLE OF INVENTION: CARBOXYPEPTIDASE B
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00995
; FILING DATE: 25-JAN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 927 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..927
; PCT-US96-00995-5

Alignment Scores:
Pred. No.: 6,37e-67 Length: 927
Score: 610.00 Matches: 126
Percent Similarity: 60.50% Conservative: 44
Best Local Similarity: 44.84% Mismatches: 71
Query Match: 33.93% Indels: 41
DB: 5 Gaps: 5

US-09-980-881A-3 (1-338) x PCT-US96-00995-5 (1-927)
QY 93 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 112
DB 1 GCAAGTGGACACAGCTACCAAGTACAACTGGAAACGATGAGCGCTGATTCAA 60
QY 113 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerPheGlu 132
DB 61 CAAGTTGCCACTGATATATCCCTTGTCTCAGAGCGTCAATGGACACATTGAA 120
QY 133 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 152
DB 121 GGACGTAACTGATATGCTCTCAAGATT---GGTAAACTAGACCGAATAAGCCTGCCATC 177
QY 153 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 172
DB 178 TTCATCGATTGTGTTCCATGTCAGAGAGTGGATTTCCTCGCATTCCTGAGTGTGTTT 237
QY 173 Ile----- 173
DB 238 GTGAGAGAGGCTGCTCCGTACCTATATCAAGAGATCCACATGAACAGCTTCTAGATGAA 297

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QY 174 -----GlyHis----- 175
Db 298 CTGATTTTCATGTCCTGCTGTCACATTCATGATGGCATATGCTACACCTGGACTAAG 357
QY 176 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 195
Db 358 GACAGATGTCGGAGAAAMACCCTCTACTATGCTGCAAGTCCTGCTGCTGGGTAGAC 417
QY 196 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGluValaSerSerSerCys 215
Db 418 CCCAACAGCAATTTT---AATGCTGGCTGTGTGAAGTGGAGCTTCTCGGACTCCCTGC 474
QY 216 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValaLysAlaValaSer 235
Db 475 TCTGAACCTTACTGTGGACAGCCCGACAGTGTGAAGAAAGACAAAGGCCCTGGCAGAT 534
QY 236 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 255
Db 535 TTCATCCGCAACACCTCTCCACCATCAGGCTACCTGACCATCCATCATCTACTACAG 594
QY 256 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 275
Db 595 ATGATCTCTACCTTACTTACTTATGCTACAAACTGCTGAGAACTATGAGGATTTGAAT 654
QY 276 LeuValaLysSerGluAlaValaArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 295
Db 655 GCCCTGTGAAGGTGCGCAAGAGAGCTT---GCCACTCTGCAAGGACCAAGTACAC 711
QY 296 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyr 315
Db 712 TATGGCCAGGAGCTCAACAACTATCTCTGCTGGGAGATCTACACATGGTCTTAT 771
QY 316 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValaGluLysLeuProLeu 335
Db 772 GATCAGAGGATCAAAATATCTTACTTTGAAGT---CCGGATACAGGCTTCTTGCTT 830
QY 336 Ser 336
Db 831 TCT 833
RESULT 15
US-08-696-139-3
Sequence 3, Application US/08696139
Patent No. 5672496
GENERAL INFORMATION:
APPLICANT: Fayerman, Jeffrey T.
APPLICANT: Greenen, David P.
APPLICANT: Hersberger, Charles L.
APPLICANT: Larson, Jeffrey L.
APPLICANT: Steiner, Jane L.
TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: Indiana
COUNTRY: United States of America
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,139
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,258
FILING DATE: 16-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-8681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 276-0756
TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..921
US-08-696-139-3

Alignment Scores:

Pred. No.:	2,096-63	Length:	921
Score:	582.00	Matches:	117
Percent Similarity:	59.47%	Conservative:	40
Best Local Similarity:	44.32%	Mismatches:	67
Query Match:	32.37%	Indels:	40
DB:	1	Gaps:	5

US-09-980-881a-3 (1-338) x US-08-696-139-3 (1-921)

QY 98 TYRGLUGINTYRHisSerLeuAsnGlnIleTyrSerTrpIleGluPheIleThrGluArg 117
Db 16 TATGAGAACTACAAACATCGGAAAGCATGAGCGCTTGAGTACAAACAGTCCAGTGAA 75
QY 118 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 137
Db 76 AATCCAGACCTCATCTCTGACAGACCATCGAGACTACTTTTGAAGAAACAATATATAC 135
QY 138 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 157
Db 136 CTCCTCAAGGTT---GGCAACCTGGACCAATTAAGCTGCAATTTTATGAGCTGTGT 192
QY 158 IleHisAlaArgLysTrpIleSerProAlaPheCysLeuTrpPheIle----- 173
Db 193 TTCATATGCCAGAGATGATTTCCCATGATTTTCCAGTGGTTTGTGAGAGAGCTGTT 252
QY 173 ----- 173
Db 253 CTCACCTATGATATAGAGATCACATGACAGAAATTCCTCAACAGCTAGACTTTATGTC 312
QY 174 -----GlyHis-----AsnArgMetTrpArg 180
Db 313 TTGCTGTGCTCATATATGATGGCTACATCTACACCTGGACCAAGACCAAGATGTGGAGA 372
QY 181 LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe 200
Db 373 AAGACCCGCTTACCAATGCTGGAACTACCTGCATTTGGACAGACCCCAACAGAAATTTT 432
QY 201 AlaSerLysHisTrpCysGluGluGluValaSerSerSerSerCysSerGluThrTyrCys 220
Db 433 ---GATGCTGGGTGTGACAACTGAGCTCTTACAGACCCCTGGATGAGACCTTACTGT 489
QY 221 GlyLeuTyrProGluSerGluProGluValaLysAlaValaSerPheLeuArgArgAsn 240
Db 490 GGATGTGCTGCGAGAGTGTGAAGAAAGACAGAGGCCCTGGCTGATTTTATACGCAACAG 549
QY 241 IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValaPhePro 260
Db 550 CTCCTCTCATCAAGCATATACCTGACGATCCATCATCTACACAGATGATCTACTACCT 609
QY 261 TyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSerLeuValaLysSerGlu 280
Db 610 TATTCCTATGATTTACAAACTCCCGAGAACATGCTGATGTAATTAACCTGGCTAAGGCT 669

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GenCore version 5.1.4-p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: May 19, 2003, 03:14:57 ; Search time 23.9746 Seconds
(without alignments)
3146.770 Million cell updates/sec

Title: US-09-980-881a-4
Perfect score: 1338
Sequence: 1 ASASYEQXHSNLEIYSWIE.....IKYFTSNPVEKTLPLSLK 246

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 441362 segs, 153338381 residues
Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB-issued.patents.NA -OFMT-fastp -SUFFIX-p2n.rn1 -MINMATCH-0.1 -LOOPEL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR SCORE-pct -THR MAX-100 -THR MIN-0 -ALIGN-15
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-NO_XLPEXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THEADS-1 -XGAPOP-10 -XGAPEXT-0.5 -Fgapop-6 -Fgapext-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT=7

Database : Issued Patents.NA.*
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5: /cgn2_6/prodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1272	95.1	1749	1	US-07-649-591B-2
4	1272	95.1	1749	1	US-08-277-540-2
5	1272	95.1	1749	1	US-08-430-787A-2
6	610	45.6	927	2	US-08-782-760-5
7	610	45.6	927	5	PCT-US96-0099-5
8	582	43.5	921	1	US-08-696-139-3
9	582	43.5	1215	1	US-08-696-139-1
10	567	42.4	999	2	US-08-860-882A-67
11	567	42.4	999	2	US-09-011-769A-50
12	567	42.4	1053	2	US-08-860-882A-64

13	567	42.4	1053	4	US-09-011-769A-46	Sequence 46, Appl
14	567	42.4	1263	2	US-08-860-882A-56	Sequence 56, Appl
15	567	42.4	1263	4	US-09-011-769A-38	Sequence 38, Appl
16	567	42.4	1284	2	US-08-860-882A-71	Sequence 71, Appl
17	567	42.4	1284	2	US-09-011-769A-55	Sequence 55, Appl
18	560	41.9	1059	2	US-08-860-882A-74	Sequence 74, Appl
19	560	41.9	1059	4	US-09-011-769A-59	Sequence 59, Appl
20	559	41.8	1059	2	US-08-860-882A-77	Sequence 77, Appl
21	559	41.8	1059	4	US-09-011-769A-63	Sequence 63, Appl
22	556.5	41.6	1311	4	US-09-675-305-8	Sequence 9, Appl
23	549	41.0	1870	4	US-09-171-945-112	Sequence 112, App
24	549	41.0	2154	4	US-09-171-945-124	Sequence 124, App
25	525.5	39.3	2128	4	US-09-675-305-13	Sequence 13, Appl
26	492	36.8	1200	4	US-09-710-099-7	Sequence 7, Appl
27	471.5	35.2	1050	4	US-09-675-305-11	Sequence 11, Appl
28	465.5	34.8	1257	3	US-08-640-906-1	Sequence 1, Appl
29	465.5	34.8	1257	4	US-09-395-936-1	Sequence 1, Appl
30	465.5	34.8	1311	4	US-09-710-099-5	Sequence 5, Appl
31	459	34.3	1251	3	US-08-640-906-3	Sequence 3, Appl
32	459	34.3	1251	4	US-09-395-936-3	Sequence 3, Appl
33	405.5	30.3	945	4	US-09-710-099-11	Sequence 3, Appl
34	405.5	30.3	945	4	US-09-710-099-11	Sequence 11, Appl
35	403.5	30.2	2247	4	US-09-710-099-15	Sequence 15, Appl
36	379	28.3	1056	4	US-09-710-099-1	Sequence 1, Appl
37	379	28.3	1056	4	US-09-710-099-9	Sequence 9, Appl
38	356	26.6	55827	4	US-09-813-133A-3	Sequence 3, Appl
39	325.5	16.9	741	4	US-09-675-305-5	Sequence 5, Appl
40	198.5	14.8	629	4	US-09-280-116-128	Sequence 28, App
41	169.5	12.7	515	4	US-08-998-416-125	Sequence 125, App
42	163	12.2	591	4	US-09-331-709-2	Sequence 2, Appl
43	104.5	7.8	673	4	US-09-280-116-93	Sequence 93, Appl
44	96.5	7.2	2382	4	US-09-641-741-1	Sequence 1, Appl
45	96.5	7.2	2719	3	US-08-706-216-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-813-133A-1
Sequence 1, Application US/09813133A
Patent No. 6453294
GENERAL INFORMATION:
APPLICANT: GAN, Weiniu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
FILE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: US09813133A
FILE REFERENCE: CLO01173
CURRENT APPLICATION NUMBER: US/09/813, 133A
CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1625
TYPE: DNA
ORGANISM: Human
US-09-813-133A-1

Alignment Scores:

Pred. No.: 4.77e-153 Length: 1625
Score: 1289.50 Matches: 244
Percent Similarity: 92.42% Conservative: 0
Best Local Similarity: 92.42% Mismatches: 2
Query Match: 96.38% Indels: 18
DB: 4 Gaps: 1

US-09-980-881A-4 (1-246) x US-09-813-133A-1 (1-1625)

QY 1 AAlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
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DB 359 GCCTCGCATCTGCTACTATGACACGATCATCTACCAATGAATTTATCTTGATTAAG 418
|||||
QY 21 PhellierhGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
|||||

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Db 419 TTTATACCTGAGAGGACATCTGATATGCTTACAAAAATCCACATTCATTCATTTGAG 478
Qy 41 LYSTYRPROLEUITYFVALLEULYSVALSERGLYSGIUGINTHRLALASANAILE 60
Db 479 AAGTACCACACTCTATGTTTAAAGSTTTCTGAAAAGACAGACCAAAAATGCCATA 538
Qy 61 TTPILASPCYSGLYLLEHISALAARGLUITRPILESERPROALAPHECYSLLEUTRPH 80
Db 539 TGGATTGACTGTGGAATCCATGACGAGAAATGATGATCTCTCTGCTTCTGCTGTGCTC 598
Qy 81 ILEGLYHISANARGMETTRPAIRGLYSANARGSERPHERYALASANASHISCYSILE 100
Db 599 ATAGGCCATATTCGAATGTGAGAAAGAACCGTTCTTTATGGAACAACATTCGATC 658
Qy 101 GLYTHRASPLeuAAsnArgAsnPheAlaSerLysHisTrpCysGIUGLUGLYALASeSer 120
Db 659 GGAACAGACCTGATAGAACCTTGCTTCCAAACAGTGTGAGGAAGGTGCATTCAGT 718
Qy 121 SerSerCysSerGIUHTYRYSGLYLEUTYRPROGLUSERGIUProGLUVALLYSALA 140
Db 719 TCCCATGCTCGGAACCTACTGCTGACTTATCTGAGTCAGAACAGAGTGAAGCA 778
Qy 141 VALAlaSerPheLeuAArgAsnIleAsnGlnIleLysAlaTyrlleSerMetHisSer 160
Db 779 GTGCTTGCTTTCTTGAGAGAAATATACACAGATTAAACCATATCATCATGCAATTC 838
Qy 161 TYSerGlnHisIleValPheProTYSerTYRThrArgSerLysSerLysAspHisGlu 180
Db 839 TACTCCAGCATATAGTGTTCATTCCTATACACAGATAAACCAAGACATGAG 898
Qy 181 GluLeuSerLeuValAlaSerGluAlaValAlaIleGluLysThrSerLysAsnThr 200
Db 899 GAACGTCTCTAGAGCACTGAGCAGTCTGCTATTCAGAAAATTAATAAAATACC 958
Qy 201 ARGTYRTHRHisGlnHisGlySerGIUHTYRLeuTYRLeuAlaProGIUGLYLysAsp 220
Db 959 AGGATACACATGCGCCATGCTGACGAGAACCTTATACCTAGCTCTGAGGTGGAGCAT 1018
Qy 221 TTPLETYRAspLeuGlyLleLysTYRSerPhe----- 231
Db 1019 TGGATCTATGATTGGGCATCAATATTCGTTACATTCAGCTGAGATCGGAGCA 1078
Qy 232 -----ThrSerAnProProValGluLysLeuProLe 243
Db 1079 TACGAGTTCTGCTGCCGAGCGTTACATCAACCCACCTGAGAGAGCTTTGCCGCT 1138
Qy 243 uSerLeuLys 246
Db 1139 GTCTCTAAAA 1148

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RESULT 2
US-08-869-057-1
Sequence 1, Application US/08869057
Patent No. 5985562
GENERAL INFORMATION:
APPLICANT: Morser, Michael J
APPLICANT: Nagashima, Mariko
TITLE OF INVENTION: Method of Detecting Thrombotic Disease
TITLE OF INVENTION: Risk
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Berlex Biosciences Legal Department
STREET: 15049 San Pablo Avenue
CITY: Richmond
STATE: California
COUNTRY: USA
ZIP: 94804-0099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/869,057
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Washlien, Wendy L
REGISTRATION NUMBER: 36,301
REFERENCE/DOCKET NUMBER: 51509AUSM1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-262-5411
TELEFAX: 510-262-7095
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1272 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PUBLICATION INFORMATION:
AUTHORS: Eaton, Dan L.
AUTHORS: Malloy, Beth E.
AUTHORS: Tsai, Siao P
AUTHORS: Henzel, William
AUTHORS: Drayna, Dennis
TITLE: Isolation, Molecular Cloning, and Partial
TITLE: Characterization of a No. 5985562el Carboxypeptidase B
JOURNAL: J Biol. Chem.
VOLUME: 266
ISSUE: 32
PAGES: 21833-21838
DATE: NO. 5985562 15-1991
US-08-869-057-1

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Alignment Scores:
Pred. No.: 5,24e-151 Length: 1272
Score: 1272.00 Matches: 246
Percent Similarity: 81.73% Conservative: 0
Best Local Similarity: 81.73% Mismatches: 0
Query Match: 95.07% Indels: 55
DB: 2 Gaps: 2

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US-09-980-881a-4 (1-246) x US-08-869-057-1 (1-1272)

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Qy 1 AlAserAlaSerTYRtyrGluGlnTYRHisSerLeuAsnGluIleTYRserTrpIleGlu 20
Db 343 GCCTCCGACATCGTACATGACAGATATCATCTCAATGAATATATTCCTTGATAGAA 402
Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 403 TTTATAACTGAGAGGACATCTGATATGCTTCAAAAAATCCACATTCGATTCATTTGAG 462
Qy 41 LYSTYRPROLEUITYFVALLEULYSVALSERGLYSGIUGINTHRLALASANAILE 60
Db 463 AAGTACCACACTCTATGTTTAAAGSTTTCTGAAAAGACAGACCAAAAATGCCATA 522
Qy 61 TTPILASPCYSGLYLLEHISALAARGLUITRPILESERPROALAPHECYSLLEUTRPH 80
Db 523 TCGATTGACTGTGGAATCATGATCCAGAGATGATCTCTCTGCTTGTGCTGTGCTGCTC 582
Qy 81 ILEGLYHIS----- 83
Db 583 ATAGGCCATATTCGAATTCATGATGAGTAATAGGCAATATACCAATCTCTGAGCTT 642
Qy 83 ----- 83
Db 643 GTGATTTCTATGTTATACCGGTGCTTATGTGACGGTTATGACTCATGGAAGAAAG 702
Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTYRAlaAsnAsnHisCysIleGlyThrAsp 103
Db 703 AATCGAATGTGAGAAAGAACCGTTCTTTATGGAACATCATTCGATGGAACAGAC 762
Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGIUGLUGLYALASeSerSerSerCys 123

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Db 763 CTGAATAGCACTTCCTCCAAACACCTGGTGTGAGGAAGTGACATCCAGTTCCTCATGC 822
OY 124 SerGluThrTyrcysglyleuTyrrProgluSerGluProgluValIysAlaValAsn 143
Db 823 TCGGAACCTACTGTGAGACTTTATCTGTGAGTCAAGAACCGAAGTGAAGCAGTGGCTAGT 882
OY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrlIleSerMetHisSerTyrrSerGln 163
Db 883 TTCTGAGAGAAGAAATATCAACAGATTAAAGCATATCAGCATGATTCATCTCCAG 942
OY 164 HisIleValPheProTyrrSerTyrrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 943 CATATAGTGTTCATATTCCTATACAGAGATAAAGCAAGACCATAGAGAACTGTCT 1002
OY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrrThr 203
Db 1003 CTAGTAGCCAGGAGAGAGAGAGTGTGCTATGAGAAAACAGTAAATATCCAGGTATACA 1062
OY 204 HisGlyHisGlySerGluThrLeuTyrrLeuAlaProGlyGlyLysAspTrpIleTyrr 223
Db 1063 CATGCCATGCTCAGAAACCTTATACCTAGCTCTGGAGTGGGAGCATTTGATCTAT 1122
OY 224 AspleuGlyIleLysTyrrSerPhe----- 231
Db 1123 GATTTGGGATCAAAATATTGTTTACATTTGAATTCGAGATACGGGCACATACGATTC 1182
OY 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeuTyrr 246
Db 1183 TTGCTGCCGAGCGCTTACTATCAACCCAGCTGTAGAGAGCTTTGCCGCTGTCTATAA 1242
OY 246 s 246
Db 1243 A 1243

RESULT 3
US-07-649-591B-2.
Sequence 2, Application US/07649591B
Patent No. 5206161
GENERAL INFORMATION:
APPLICANT: Dennis Drayna and Daniel Eaton
TITLE OF INVENTION: No. 5206161el Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/649, 591B
FILING DATE: 19910201
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28, 616
REFERENCE/DOCKET NUMBER: 689
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1749 bases
TYPE: NUCLEIC ACID

STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: hybridization probe
LOCATION: 133 to 178
IDENTIFICATION METHOD:
OTHER INFORMATION:
FEATURE:
NAME/KEY: potential clip site
LOCATION: 380 to 382
IDENTIFICATION METHOD:
OTHER INFORMATION:
NAME/KEY: signal sequence
LOCATION: 41 to 106
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-07-649-591B-2

Alignment Scores:
Pred. No.: 8, 77e-151
Score: 1272.00
Percent Similarity: 81.73%
Best Local Similarity: 81.73%
Query Match: 95.07%
DB: 1
Matches: 1749
Conservative: 246
Mismatches: 0
Indels: 55
Gaps: 2

US-09-980-881a-4 (1-246) x US-07-649-591B-2 (1-1749)

OY 1 AlaSerAlaSerTyrrTyrrGluGlnTyrrHisSerLeuAsnGluIleTyrrSerTrpIleGlu 20
Db 383 GCCTCCGATCGTACTATATACAGTATCATCTACTAAATCAATCTATTCCTGGATAGAA 442
OY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
Db 443 TTTATACAGAGAGCATCTCTGATATGCTTACAAATATCCATTCGATTCCTATTTGAG 502
OY 41 LysTyrrProLeuTyrrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
Db 503 AAGTACCACCTATGTTTAAAGGTTTCTGGAAAGAACAAACAGCCAAATATGTCATTA 562
OY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 563 TCGATTGACGTGGATCATCATGCCAGAGATGATCTCTGCTTTCGCTTGTGTTTC 622
OY 81 IleGlyHis----- 83
Db 623 ATAGCCATATTAATCAATTCTATGGGATATAGGCCAATATACCAATCTCTGAGGCTT 682
OY 83 ----- 83
Db 683 GTGGAATTTCATGTATATGCCGCGTGTAAATGTGAGCGTTATGATCACTACATGGAAG 742
OY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrrAlaAsnAsnHisCysIleGlyThrAsp 103
Db 743 AATCGAATGTGGAGAAAGAACCGTCTTCTATGCAACAATCATATGATCCGAAACAGAC 802
OY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
Db 803 CTGAATAGGAACTTCTCTCCAAACACTGTGTGAGAGAGGTCCATCCAGTTCCTATGC 862
OY 124 SerGluThrTyrcysglyleuTyrrProgluSerGluProgluValIysAlaValAsn 143
Db 863 TCGGAACCTACTGTGAGACTTTATCTGTGAGTCAAGAACCGAAGTGAAGCAGTGGCTAG 922
OY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrlIleSerMetHisSerTyrrSerGln 163
Db 923 TTCTGAGAGAAGAAATATCAACAGATTAAAGCATATCAGCATGATTCATCTCCAG 982
OY 164 HisIleValPheProTyrrSerTyrrThrArgSerLysSerLysAspHisGluGluLeuSer 183
Db 983 CATATAGTGTTCATATTCCTATACAGAGATAAAGCAAGACCATAGAGAGTGTCT 1042

QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
 |||||||
 Db 1043 CTAGTACCGACGTGAAGAGTTCGTCATATGAGAAACTGTAATAATACAGGTATACA 1102
 QY 204 HisGlyHisGlySerGluThrLeuAlaProGlyGlyAspAspTyrIleTyr 223
 |||||||
 Db 1103 CATGGCCATGGCTCAGAAACCTATACCTAGCTCTGAGCTGGGAGCATTTGATCTAT 1162
 QY 224 AspleuglyIleLysTyrSerPhe----- 231
 |||||||
 Db 1163 GATTGGGCAATCAATATTGCTTACATTCGAACCTTCGAGATACGGGCATACGATTC 1222
 QY 232 -----ThSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
 |||||||
 Db 1223 TTGCTGCCGAGCGTTACATCAACACCTGTAGAGAACCTTTGGCGCTGTCTCTAAA 1282
 QY 246 s 246
 Db 1283 A 1283
 RESULT 4
 US-08-277-540-2
 : Sequence 2, Application US/08277540
 : Patent No. 5474901
 : GENERAL INFORMATION:
 : APPLICANT: Drayna, Dennis T., Eaton, Dan L.
 : TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase
 : NUMBER OF SEQUENCES: 8
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genentech, Inc.
 : STREET: 460 Point San Bruno Blvd
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: patlin (Genentech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/277,540
 : FILING DATE: 19-JUL-1994
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/167727
 : FILING DATE: 15-DEC-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/959944
 : FILING DATE: 14-OCT-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/649591
 : FILING DATE: 01-FEB-91
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hasak, Janet E.
 : REGISTRATION NUMBER: 28,616
 : REFERENCE/DOCKET NUMBER: 689D1C1D1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415/225-1896
 : TELEFAX: 415/952-9881
 : TELEX: 910/371-7168
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1749 bases
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-277-540-2
 Alignment Scores:
 Pred. No.: 8.77e-151 Length: 1749
 Score: 1272.00 Matches: 246
 Percent Similarity: 81.73% Conservative: 0

Best Local Similarity: 81.73% Mismatches: 0
 Query Match: 95.07% Indels: 55
 DB: 1 Gaps: 2
 US-09-980-881a-4 (1-246) x US-08-277-540-2 (1-1749)
 QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
 |||||||
 Db 383 GCCTCCGACATCGTACTATGACATGACATGATCACTAAATGAATCTATTCTTGATAGAA 442
 QY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
 |||||||
 Db 443 TTATATACGACAGGCATCCTGATATGCTTACAAAATCCACATTGATCTCATTTGAG 502
 QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
 |||||||
 Db 503 AAGTACCACACTCATGTGTTTAAAGCTTCTGGAAGAAAGAACAAACAGCCAAATATGCCATA 562
 QY 61 TrpIleAspCysGlyTyrIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
 |||||||
 Db 563 TGGATTGACTGTGGCAATCCATGCCAGAGATGATCTCTGCTTCTGTGGTTC 622
 QY 81 IleGlyHis----- 83
 |||||||
 Db 623 ATAGGCCATATATCACTAATTATGAGCATATATAGGCAATATACCAATCTCTGAGGCTT 682
 QY 83 ----- 83
 |||||||
 Db 683 GTGATTTCTATGTAATGCGGCTGTATATGACGGTTATGACTACTCATGAGAAAG 742
 QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnHisCysIleGlyThrAsp 103
 |||||||
 Db 743 AATCGAATGTGAGAGAAAGACCGTTCTTTCTATGCGAACATCATTTGATCGAGACAGAC 802
 QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
 |||||||
 Db 803 CTGAATAGAGAACTTGCTCCAAACACTGTGTGAGAAAGGTGATCCAGTTCCCTCATGC 862
 QY 124 SerGluThrTyrCysGlyLeuLysProGluSerGluProGluValAlaValAlaSer 143
 |||||||
 Db 863 TCGGAACCTACTGTGCACTTTATCTGAGTCAGAACCAAGAGTAAAGGCAAGTGGCTAGT 922
 QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
 |||||||
 Db 923 TTCTTGAGAGAAATATACACAGATTAAGCATATACATGATCTACTCTCCAG 982
 QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
 |||||||
 Db 983 CATATAGCTTTCCATATTCCTATACAGCAAGTAAAGCAAAAGCATGAGCAACTGTCT 1042
 QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
 |||||||
 Db 1043 CTAGTACCGACGTGAAGAGTTCGTCATATGAGAAACTGTAATAATACAGGTATACA 1102
 QY 204 HisGlyHisGlySerGluThrLeuAlaProGlyGlyAspAspTyrIleTyr 223
 |||||||
 Db 1103 CATGGCCATGGCTCAGAAACCTTATACCTAGCTCTGAGCTGGGAGCATTTGATCTAT 1162
 QY 224 AspleuglyIleLysTyrSerPhe----- 231
 |||||||
 Db 1163 GATTGGGCAATCAATATTGCTTACATTCGAACCTTCGAGATACGGGCATACGATTC 1222
 QY 232 -----ThSerAsnProProValGluLysLeuLeuProLeuSerLeuLys 246
 |||||||
 Db 1223 TTGCTGCCGAGCGTTACATCAACACCTGTAGAGAACCTTTGGCGCTGTCTCTAAA 1282
 QY 246 s 246
 Db 1283 A 1283
 RESULT 5
 US-08-430-787A-2
 : Sequence 2, Application US/08430787A

Patent No. 5593674
GENERAL INFORMATION:
APPLICANT: Drayna, Dennis T., Paton, Dan L.
TITLE OF INVENTION: No. 5593674e1 Plasma Carboxypeptidase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430.787A
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/277,540
FILING DATE: 19-JUL-1994
APPLICATION NUMBER: 08/167727
FILING DATE: 15-DEC-1993
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/959944
FILING DATE: 14-OCT-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/649591
FILING DATE: 01-FEB-91
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 689D1C1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1749 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-430-787A-2
Alignment Scores:
Pred. No.: 8.77e-151 Length: 1749
Score: 1272.00 Matches: 246
Percent Similarity: 81.73% Conservative: 0
Best Local Similarity: 81.73% Mismatches: 55
Query Match: 95.07% Indels: 55
DB: 1 Gaps: 2
US-09-980-881A-4 (1-246) x US-08-430-787A-2 (1-1749)
QY 1 AlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 383 GCCTCCGCATGCTACTATGACACAGTATCATCACTAATGAATCTATCTTGGATAGAA 442
QY 21 PheIleThrGluArgHisProAspMetLeuThrIleHisIleGlySerSerPheGlu 40
DB 443 TTTATACCTGAGAGGACCTGATATGCTTACAAAATCCACATTGATCCTCATTTGAG 502
QY 41 LysTyrProLeuTyrValIleuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 503 AAGTACCCACCTATGTTTAAAGCTTCTGGAAGAAACAAACAGCCAAATATGCCATA 562
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
DB 563 TGGATTGACTGTGGAATCCATGCCAGAGAAATGATCTCTCCGCTTCTGCTTGGGTTTC 622

QY 81 IleGlyHis-----83
DB 623 ATAGGCCATATATCACTAATTCATGGATTAATAGGCAATATACCAATCTCTAGAGCTT 682
QY 83 -----83
DB 683 GTGATTTCTATGTTATGCGCGGTGTTAATGTGACGGGTATGACTCATGAGAAAAG 742
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysTrpIleGlyThrAsp 103
DB 743 AATCGAATGTGAGAAAGAACCGTTCTTCTATGCGAACATCATTCGATGGAACAGAC 802
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 803 CTGATAGCAACTTGTCTTCCCAACACACTGCTGTGAGAAAGTGCAATCCAGTCCCATGC 862
QY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
DB 863 TCGGAACCTACTGTGACTTATCTCTGAGTCAGAACAGAGAGTGAAGCAGCTGCTAGT 922
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 923 TTTCTGAGAGAAATATACACCGATTAAGCATACATCAGCATTCATTCATCTCCAG 982
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 983 CATATAGTCTTCCATATTCCTATACAGCAAGTAAAGCAAGACCATGAGGAACTGCT 1042
QY 184 LeuValAlaSerGluAlaValAlaIleGlyLysThrSerLysAsnThrArgTyrThr 203
DB 1043 CTAGTAGCCAGAGAGAGAGCTGCTGCTATGAGAAACAGTAAATAACAGTATAC 1102
QY 204 HisGlyHisGlySerGluThrLeuTyrIleuAlaProGlyGlyGlyAspAspTrpIleTyr 223
DB 1103 CATGCCCATGCTGCAAGAACCTTATATACCTAGCTCTGAGGTGGAGCAGATTGATTA 1162
QY 224 AspLeuGlyIleLysTyrSerPhe-----231
DB 1163 GATTTGGCGCATCAATATTCGTTTACAAATTCGACACTTCAGATACGGGCACATACGATT 1222
QY 232 -----ThrSerAsnProProValGluLysLeuLeuProLeuSerLeu 246
DB 1223 TTGCTGCCGAGAGCTTACATCAAAACCTGTAGAGAAAGCTTTGGCGCTCTCTAAA 1282
QY 246 s 246
DB 1283 A 1283
RESULT 6
US-08-782-760-5
Sequence 5, Application US/08782760
Patent No. 5948668
GENERAL INFORMATION:
APPLICANT: Hartman, Jacob
APPLICANT: Fulga, Netia
APPLICANT: Mendelovitch, Simona
APPLICANT: Gorecki, Marian
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/782,760
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,233
FILING DATE: 25-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0336/43847
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..927
US-08-782-760-5
Alignment Scores:
Pred. No.: 1,666-67 Length: 927
Score: 610.00 Matches: 126
Percent Similarity: 60.50% Conservative: 44
Best Local Similarity: 44.84% Mismatches: 71
Query Match: 45.59% Indels: 41
DB: 2 Gaps: 5
US-09-980-881a-4 (1-246) x US-08-782-760-5 (1-927)
QY 1 AAlaSerAlaSerTyrTyrGluGlnTyrHisSerLeuAsnGlnIleTyrSerTrpIleGlu 20
DB 1 GCAGAGTGACACAGCACTACACAGCTACACAGCTACACAGCTACACAGCTACACAG 60
QY 21 PheIleThgIuArgHisProAspMetLeuThrLysIleHisIleGlySerPheGlu 40
DB 61 CAAGTTGCCACTGATATATCAAGACCTTGTCACTCAAGCGCTCATTTGAAACCATTTGAA 120
QY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 121 GGACGTAACATGATATGCTCAAGATT---GGTAAACTAGACCGAATAGACCTGCCATC 177
QY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
DB 178 TTCATCGATTGTGGTTCCATGCAAGAGAGTGATTTCTCGCATTTCTGTGAGTGGTTT 237
QY 81 Ile----- 81
DB 238 GTGAGAGAGCGTGTCCGTAATCAAGATCCACATGAACAGCTTCTAGATGAA 297
QY 82 -----GLYHis----- 83
DB 298 CTGGAATTTCTATGTTCTGCTGTGGTCAACATTTGATGGCTATGTCTACACCTGGACTAAG 357
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 358 GACAGAAATGTGAGAAAAACCGCTCTACTATGCTGGAAGTTCCGCTTGGGTGAGAC 417
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 418 CCCAAGCAGGAATTTT---AATGCTGGCTGGTGTGAAGTGGAGCTTTCGGAGTCCCTTC 474
QY 124 SerGluThrTyrCysGlyLeuTyrTrpGluSerGluProGluValLysAlaValAlaSer 143
DB 475 TCTGAACCTTACTGTGTGACCGACCCCAAGAGTCTGAAAAAGACAAAGGCCCTGGCAGAT 534

QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 535 TTCATCCGACACACACTCTCCACCATCAAGCCTTACCTACCATCACCATCTACACG 594
QY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
DB 595 ATGATGCTCTACCTTACTTACCTATGACTCAAAAGTCCCTGAGAACATATGAGGATTTGAT 654
QY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 655 GCCCTGTGTAAGCTCGGCAAGAGCTT---GCCACTCTGCATGGCCCAAGTACACA 711
QY 204 HisGlyHisGlySerGluThrLeuTyrLeuAlaProGlyGlyLysAspTrpIleTyr 223
DB 712 TATGGCCCAAGACACTCAACAATCTATCTGCTGCTGGGGATCTGACGACGTGCTTAT 771
QY 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuAspProLeu 243
DB 772 GATCAGGAAATCAAAATATTCCTTACTTTGAAGT---CCGGATACAGCCTTCTTGGCTT 830
QY 244 Ser 244
DB 831 TCT 833
RESULT 7
PCT-US96-00995-5
Sequence 5, Application PC/TUS960095
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: PRODUCTION OF ENZYMATICALLY ACTIVE
NUMBER OF INVENTION: CARBOXYPEPTIDASE B
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00995
FILING DATE: 25-JAN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0336/43847-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 927 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..927
PCT-US96-00995-5
Alignment Scores:
Pred. No.: 1,666-67 Length: 927
Score: 610.00 Matches: 126

Percent Similarity: 60.50% Conservative: 44
 Best Local Similarity: 44.84% Mismatches: 71
 Query Match: 45.59% Indels: 41
 DB: 5 Gaps: 5

US-09-980-881a-4 (1-246) x PCT-US96-00995-5 (1-927)

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OY 1 AAlaserAlaserTyrTrpGlnGlnTyrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
DB 1 GCAAGTGCACACAGCTACACCAAGTACACCACTGGGAACGATTGAGCGTGGATTCAA 60
OY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 61 CAAGTGCACACAGCTACACCAAGCTTGTCTACTCAGACGCTCATTTGGAAACCAATTGAA 120
OY 41 LysTyrProLeuValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 121 GCACGTACACATGATGCTCTCAAGATT--GGTAAACTAGACCAATAGCGCTGCATC 177
OY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
DB 178 TTCATCGATTTGGTTTTCATGCAAGAGGTGATTTCCTGCATTTCTGTGAGTGGTTT 237
OY 81 Ile----- 81
DB 238 GTGAGAGAGGCTGCTCCGTACTATATCAAGATCCACATGAAACAGCTTGATGAA 297
OY 82 -----GlyHis----- 83
DB 298 CTGATTTCTATGTTCTGCTGCTGTGTCACATGATGATGCTATGCTTACACCTGGAGTAAG 357
OY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 358 GACAGATGTCGAGAGAAACCCGCTCTACTATAGCTGCGAAGTTCCTGGTGTAGAC 417
OY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
DB 418 CCCAACAGGAATTTT--AATGCTGCTGCTGGAAGTGGAGCTTCTGGAGTCCCTGC 474
OY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaLysAlaSer 143
DB 475 TTGTAATCTACTGTGGACACCCCGAGCTCTGAAAAGAGCAAGAGCCCTGGGAGAT 534
OY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
DB 535 TTCATCGCAGCAACACCTCCACCACTCAAGGCTTACCATCCATCATACTACAG 594
OY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGluLeuSer 183
DB 595 ATGATGCTCTACCTTACTCTTACTGACTCAAACTGCTGAGAACTATAGAGAAATGAAAT 654
OY 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyrThr 203
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OY 224 AspLeuGlyIleLysTyrSerPheThrSerAsnProProValGluLysLeuProLeu 243
DB 772 GATCAGGAGAAATATATCTTACTTCTTGAACCT--CCGGGATACAGGCTTCTTGGCTT 830
OY 244 Ser 244
DB 831 TCT 833

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RESULT 8
 US-08-696-139-3
 : Sequence 3, Application US/08696139
 : Patent No. 5672496
 : GENERAL INFORMATION:
 : APPLICANT: Fayerman, Jeffrey T.

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? APPLICANT: Greenen, David P.
? APPLICANT: Hersberger, Charles L.
? APPLICANT: Larson, Jeffrey L.
? APPLICANT: Sterner, Jane L.
? APPLICANT: Zhang, Haichao
? TITLE OF INVENTION: DNA SEQUENCES ENCODING PORCINE
? NUMBER OF INVENTIONS: 6
? NUMBER OF SEQUENCES: 6
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Eli Lilly and Company
? STREET: Lilly Corporate Center
? CITY: Indianapolis
? STATE: Indiana
? COUNTRY: United States of America
? ZIP: 46285
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/696,139
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/153,258
? FILING DATE: 16-NOV-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Gaylo, Paul J.
? REGISTRATION NUMBER: 36,808
? REFERENCE/DOCKET NUMBER: X-8681
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (317) 276-0756
? TELEFAX: (317) 276-3861
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 921 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..921
? US-08-696-139-3
? Alignment Scores:
? Pred. No.: 5.7e-64 Length: 921
? Score: 582.00 Matches: 117
? Percent Similarity: 59.47% Conservative: 40
? Best Local Similarity: 44.32% Mismatches: 67
? Query Match: 43.50% Indels: 40
? DB: 1 Gaps: 5
? US-09-980-881a-4 (1-246) x US-08-696-139-3 (1-921)
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DB 16 TATGAGAGTACACACAGCTGGGAACGATCGAGCGTTGACTGCAATTCACCACTGAA 75
OY 26 HisProAspMetLeuThrLysIleHisIleGlySerSerPheGluLysTyrProLeuTyr 45
DB 76 AATCCAGACCTCATCTCTGCGACAGCCATCGCACTGCAATTTTACGAAACAATATATAC 135
OY 46 ValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIleTrpIleAspCysGly 65
DB 136 CTCCTCAAGGTT--GGCAAACTGGAGCCAAATTAACCTTGCAATTTTCATGAGCTGTGT 192
OY 66 IleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPheIle----- 81
DB 193 TTCATGCCAGAGAAATGATTTCCATGCAATTTGGCACTGTTGTGAGAGAGCTGTT 252
OY 81 ----- 81

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Qy	82	-----GlyHis-----AsnArgMetTParG	88
Db	313	TTGCCTGTGCTCAATATTGATGGCTAGACTTACACCTGGACAGAAAGCAACAAATCTGGAGA	3727
Qy	89	LysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAspLeuAsnArgAsnPhe	1081
Db	373	AAGACCGCTCTACCAAAATGCTGGAAACTACCTGATTTGGACAGAGCCCAACAGAAATTTT	4322
Qy	109	AlaSerLysHisThrPcysGluGluGlyAlaSerSerSerCysSerGluThrTyrCys	1288
Db	433	---GATGCTGGGTGGTGCAACAGTCGAGACCTCTACACACCCCTGCGTAGAGACTTACTGT	4891
Qy	129	GlyLeuTyrProGluSerGluProGluValLysAlaValAlaSerPheLeuArgArgAsn	1481
Db	490	GGATCTGCTGCAGAGTGTGAAAAAGAGACCAAGGCCCTGCTGATTTTATACCAACACAC	5491
Qy	149	IleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlnHisIleValPhePro	1681
Db	550	CTCTCTCCATTCAAAGCATTAACCTTACAGATCCACATCACTACACGATGATACCTTACCT	6091
Qy	169	TyrSerTyrThrArgSerLysSerLysAspHisGluLeuSerLeuValAlaSerGlu	1881
Db	610	TATTCCTATGATTACAAACCTCCCGAGAACATCTGATGTAATACCTGGCTAAGCT	6691
Qy	189	AlaValAlaGlnAlaIleGluLysThrSerLysAsnThrArgTyrThrHisGlyHisGlySer	2081
Db	670	GCCGGAAGAAAGACTT--GCTACACTGTATGGCCACCAAGTACATACGCGCCAGAGAGCT	7261
Qy	209	GluThrLeuTyrLeuAlaProGluGlyGlyAspAspPrIleTyrIleAspLeuGlyIleLys	2281
Db	727	ACAAACAATCTATCCGCTGCTGGGGGCTGTGATGATGACTGGGCTTATATGACCAAGGATCAAA	7861
Qy	229	TySerPheThr 232	
Db	787	TATTCCTTCACCC 798	

```

? NAME: Gaylo, Paul J.
? REGISTRATION NUMBER: 36, 808
? REFERENCE/DOCKET NUMBER: X-8681
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (317) 276-0756
? TELEFAX: (317) 276-3861
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1215 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1215
? OS-08-696-139-1

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Db 964 GCCGGAAGACTT---GCTACACTGTATGGCACCAGTACACATACAGCCAGACT 1020
 Oy 209 GlturhLeuTyrlLeuAlaProglyLyglYAspAspTPIleTyAspLeuGlylyls 228
 Db 1021 ACACAAATCTATCTGCTGCTGGGGCTCTGTATGACTGGCTTATGACCAAGAAATCAAA 1080
 Oy 229 TySerPheThr 232
 1081 TATTCCTTACC 1092
 RESULT 10
 US-08-860-882A-67
 : Sequence 67, Application US/08860882A
 : Patent No. 5985281
 : GENERAL INFORMATION:
 : APPLICANT: TAYLORSON, CHRISTOPHER JOHN
 : APPLICANT: EGGELTE, HENDRIKUS JOHANNES
 : APPLICANT: TARRAGONA-FIOL, ANTONIO
 : APPLICANT: RABIN, BRIAN ROBERT
 : APPLICANT: BOYLE, FRANCIS THOMAS
 : APPLICANT: HENNAM, JOHN FREDERICK
 : APPLICANT: BLAKELY, DAVID CHARLES
 : APPLICANT: MARSHAM, PETER ROBERT
 : APPLICANT: HEATON, DAVID WILLIAM
 : TITLE OF INVENTION: CHEMICAL COMPOUNDS
 : NUMBER OF SEQUENCES: 77
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: PILLSBURY, MADISON & SUTRO
 : STREET: 1100 NEW YORK AVENUE, N.W.
 : CITY: WASHINGTON
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20005
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy Disk
 : OPERATING SYSTEM: IBM compatible
 : SOFTWARE: Patent in Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/860,882A
 : FILING DATE: JUNE 23, 1997
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: DONALD J. BIRD
 : REGISTRATION NUMBER: 25,323
 : REFERENCE/DOCKET NUMBER: 9901/238653
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (202) 861-3027
 : TELEFAX: (202) 822-0944
 : TELEX: 6174627 CUSH
 : INFORMATION FOR SEQ ID NO: 67:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 999 bases
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : US-08-860-882A-67
 : Alignment Scores:
 : Pred. No.: 5.13e-62 Length: 999
 : Score: 567.00 Matches: 111
 : Percent Similarity: 58.36% Conservative: 46
 : Best Local Similarity: 41.26% Mismatches: 72
 : Query Match: 42.38% Indels: 40
 : DB: 2 Gaps: 5
 : US-09-980-881A-4 (1-246) x US-08-860-882A-67 (1-999)
 : Oy 1 AlAserAlaSerTyTyTyGluGlnTyTrHisSerLeuAsnGluIleTySerTrpIleGlu 20
 : Db 67 GCAACTGTCTACTTACGAGAGTACAAAGATGCGAAGCATTAGAGGCTTGACTCA 126

Oy 21 PheIleThrGluArgHisProaspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
 Db 127 CAAGTCCGACACAGAACATCCACCTCATCTCCGACAGTGTATGGAACCAATTTGAG 186
 Oy 41 LysTyProLeuTyValLeuLysValSerGlyLysGluInThrAlaLysAsnAlaIle 60
 Db 187 GGACCGCTATTACCTCCTGAAAGTT---GCCAAGCTGACAAATATAGCTGCCATT 243
 Oy 61 TrpIleaspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
 Db 244 TTCATGAGACTGTGTTCCATGTCAGAGAGTGATTTTCCTGCAATTCGACAGTGT 303
 Oy 81 Ile----- 81
 Db 304 GTAAGAGAGCTTTCGTAACCTATGAGCTGAGATTCACCAAGTACAGAGCTTCCACAG 363
 Oy 82 -----GlyHis----- 83
 Db 364 TTAGACTTTTATGCTCCTGCTGCTCAATATTGATGGCTACATCTACACCTGACCAAG 423
 Oy 84 AsnArgMetTrpArgLysAsnArgSerPheTyAlaAsnAsnHisCysIleGlyThrAsp 103
 Db 424 AGCCGATTTTGGAGAAGACTGCTCCACCATCTGATGATCTGATGCTGATGCGACAGAC 483
 Oy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluAlaSerSerSerCys 123
 Db 484 CCCAAGACAAATTTT---GATCTGCTGTGTGTGAATTTGGAGCCCTCGAAGACCCCTGT 540
 Oy 124 SerGluThrTyrcysGlyLeuTyProGluSerGluProGluValLysAlaValAlaSer 143
 Db 541 GATGAACCTTACTGTGAGCTCCGACAGTCTGAAAGAGACCAAGGCCCTGCTGAT 600
 Oy 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrlleSerMetHisSerTyserGln 163
 Db 601 TTCATCCGCAACAACTCTTCCATCAAGGCATCTGACATCCACTCCGATCCCA 660
 Oy 164 HisIleValPheProTySerTyThrArgSerLysSerLysAspHisGluLeuSer 183
 Db 661 ATGATGATCTACCTTACTCATATGCTTCAACATCGGAGAACAAATCTAGTTGAT 720
 Oy 184 LeuValAlaSerGluAlaValArgAlaIleGluLysThrSerLysAsnThrArgTyThr 203
 Db 721 GCCCTGGCTAAGCTAGTGTGAAGAACTT---GCCCTGCTCAGCGGACCAAGTACACA 777
 Oy 204 HisGlyHisGlySerGluThrLeuTyrlleuAlaProGlyLyglYAspAspTPIleTy 223
 Db 778 TATGCCCCGGAGCTACACAACTATCTGCTGCTGGGGCTCTGAGAGCTGGCTTAT 837
 Oy 224 AspLeuGlyIleLysTySerPheThr 232
 Db 838 GACCAAGGATCAGATATTCCTTACC 864
 RESULT 11
 US-09-011-769A-50
 : Sequence 50, Application US/09011769A
 : Patent No. 6436591
 : GENERAL INFORMATION:
 : APPLICANT: SLATER, Anthony M.
 : BLAKELY, David C.
 : DAVIES, David H.
 : HENNAM, John F.
 : HENNEQUIN, Laurent F.A.
 : MARSHAM, Peter R.
 : DOWELL, Robert I.
 : TITLE OF INVENTION: Chemical Compounds
 : NUMBER OF SEQUENCES: 87
 : CORRESPONDENCE ADDRESSES:
 : ADDRESSEE: Pillsbury Madison & Sutro, LLP
 : STREET: 1100 New York Ave., N.W.
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: U.S.A.

STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-64

Alignment Scores:
Pred. No.: 5,58e-62 Length: 1053
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-64 (1-1053)

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OY 1 AlaserAlaserTyrTyrGluGluTyrHisSerLeuasnGluTyrSerTrpIleGlu 20
DB 67 GCAACGCGTACTCTTACAGAGAGTACAACTGGGAAACGATAGAGCTTGACTCAA 126
OY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAGTCGCCACAGAGATCCAGCCCTCATCTCCGACGTGTATCGAACCACATTGGAG 186
OY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCGTATTACCTCCTGAAGGTT---GGCAAGCTGGACAAATAGACCTGCCATT 243
OY 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
DB 244 TTCATGAGACTGTGTTGTTCCATGCGACAGAGATGATTTCTCTGCAATTCGACGTGTT 303
OY 81 Ile-----GlyHis-----81
DB 304 GTAAGAGAGCTGTCTGCTACTATGAGCGTGAATCCAGTGACAGAGCTTTCGACAAAG 363
OY 82 -----82
DB 364 TAGACTTTTATGCTCCTGCCCTGCTCAATATGATGATGCTACATCAACACCTGGACCAAG 423
OY 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
DB 424 ACCCGATTTTGGAGAAAGACTCGCTCCACCACACTGATCTGATGCTGACACAGAC 483
OY 104 LeuAsnArgAsnPheAlaSerLysHisTyrCysGluGluGlnValaSerSerSerCys 123
DB 484 CCCAACGAGAAATTTT---GATGCTGTTGTTGTAATGGAGCTCTCGAACCCTCTGT 540
OY 124 SerGluThrTyrCysGlyLeuTyrProGluSerGluProGluValLysAlaValaSer 143
DB 541 GATGAACCTTACTGTGAGCTGCCGCGAGAGTGGAAAGAGACCAAGGCCCTGGCTGAT 600
OY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTyrIleSerMetHisSerTyrSerGlu 163
DB 601 TTCATCCGCAACAACTCTTCCATCAAGGCTATCTGACATCTCCTGATCTCCAA 660
OY 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluGlnLeuSer 183
DB 661 ATGATGATCTACCTTACTCATATGCTTACAAACTGGGAGAAACAATGCTGAGTTGAAT 720
OY 184 LeuValAlaSerGluAlaValaIleGluLysThrSerLysAsnThrArgTyrThr 203
DB 721 GCCCTGCTTAAAGCTACTGTGAAGACTT---GCCCTGACTGCAGCGCAACCAAGTACACA 777
OY 204 HisGlyHisIleGlySerGluThrLeuTyrLeuAlaProGlyLysAspTrpIleTyr 223
DB 778 TATGGCCCGGAGCTACACAACTATCTCTGCTGCTGGGGCTCTGACACTGGGCTTAT 837
OY 224 AspLeuGlyIleLysTyrSerPheThr 232
DB 838 GACACAGGAATCAGATATTCCTTCACC 864

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RESULT 13
US-09-011-769A-46
; Sequence 46, Application US/09011769A

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? Patent No. 6436691
? GENERAL INFORMATION:
? APPLICANT: SLATER, Anthony M.
? BLAKEY, David C.
? DAVIES, David H.
? HENNAM, John F.
? HENNEQUIN, Laurent F.A.
? MARSHAM, Peter R.
? DOWELL, Robert I.
? TITLE OF INVENTION: Chemical Compounds
? NUMBER OF SEQUENCES: 87
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Pillsbury Madison & Sutro, LLP
? STREET: 1100 New York Ave., N.W.
? CITY: Washington
? STATE: D.C.
? COUNTRY: U.S.A.
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 1.44 Mb disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: MS Word
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/011,769A
? FILING DATE: 13-Feb-1998
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/GB96/01975
? FILING DATE: 13-AUG-1996
? APPLICATION NUMBER: GB 9612295.7
? FILING DATE: 12-JUN-1996
? APPLICATION NUMBER: GB 9611019.2
? FILING DATE: 25-MAY-1996
? APPLICATION NUMBER: GB 9516810.0
? FILING DATE: 16-AUG-1995
? INFORMATION FOR SEQ ID NO: 46:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1053 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: other nucleic acid
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1047
? NAME/KEY: mat_peptide
? LOCATION: 67..1047
? SEQUENCE DESCRIPTION: SEQ ID NO: 46:
? US-09-011-769A-46
?
? Alignment Scores:
? Pred. No.: 5,58e-62 Length: 1053
? Score: 567.00 Matches: 111
? Percent Similarity: 58.36% Conservative: 46
? Best Local Similarity: 41.26% Mismatches: 72
? Query Match: 42.38% Indels: 40
? DB: 4 Gaps: 5
?
? US-09-980-881A-4 (1-246) x US-09-011-769A-46 (1-1053)
OY 1 AlaserAlaserTyrTyrGluGluTyrHisSerLeuasnGluTyrSerTrpIleGlu 20
DB 67 GCAACGCGTACTCTTACAGAGTACAACTGGGAAACGATAGAGCTTGACTCAA 126
OY 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
DB 127 CAAGTCGCCACAGAGATCCAGCCCTCATCTCCGACGTGTATCGAACCACATTGGAG 186
OY 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluGlnThrAlaLysAsnAlaIle 60
DB 187 GGACGGCGTATTACCTCCTGAAGGTT---GGCAAGCTGGACAAATAGACCTGCCATT 243

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QY 61 TrpIleAspCysGlyIleHisAlaArgIleuTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 244 TTCATGACGTGGTTCATGACCCAGACAGTGGATTTCTCGCATTTCTGCCAGTGGTTT 303
QY 81 Ile----- 81
Db 304 GTAAGAGAGCGTGTCTGACTATGAGACGTGATCCAAAGTGCAGAGACTTCTCGACAG 363
QY 82 -----GlyHis----- 83
Db 364 TTAACTTTTATGTCCTGCTGCTGCTCAATATTGATGGCTTACATCTACACCTGACCAAG 423
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTrpAlaAsnHisCysIleGlyThrAsp 103
Db 424 AGCGATTTTGGAGAAAGACTCGCTCCACCATCTAGTATCTACTGATTTGGACAGAC 483
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluAlaSerSerSerCys 123
Db 484 CCCACAGAAATTTT---GATGCTGTTGGTGTGAATTTGGAGCCTCTCGAAACCCCTGT 540
QY 124 SerGluThrTrpCysGlyLeuTrpProGluSerGluProGluValLysAlaValAlaSer 143
Db 541 GATAAACTTACTGTGACCTGCCGCGAGACTCTGAAGAAGAGACCAAGCCCTGGCTGAT 600
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGln 163
Db 601 TTCATCCGCAACAAACTCTCTTCATCAGACGATATCTGCAATATCCATCTGATCCCAA 660
QY 164 HisIleValPheProTrpSerTrpThrArgSerLysSerLysAspHisGluLeuSer 183
Db 661 ATGATGATCTACCTTCTCATATGCTTACAAACTCGGTGAAGAAATGCTGATTTGAAT 720
QY 184 LeuValAlaSerGluAlaValAlaArgAlaIleGluTrpSerLysAsnTrpArgTrpThr 203
Db 721 GCCCTGGCTAAAGCTACTGTGAAAGAACT---GCCCTACTGCGACGGCACCAAGTACACA 777
QY 204 HisGlyHisGlySerGluTrpLeuTrpLeuAlaProGlyLysAspTrpIleTrp 223
Db 778 TATGGCCCGGAGACTACAAACATCTATCTGCTGGGGGCTGTGACGACTGGGCTTAT 837
QY 224 AspleuGlyIleLysTrpSerPheTrp 232
Db 838 GACCAAGCATCATATCTCTTCAC 864

RESULT 14
US-08-860-882A-56
Sequence 56, Application US/08860882A
Patent No. 5985281
GENERAL INFORMATION:
APPLICANT: TAYLORSON, CHRISTOPHER JOHN
APPLICANT: EGGLESE, HENDRIKUS JOHANNES
APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: HENNAN, JOHN FREDERICK
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID HOW
APPLICANT: DAVIES, DAVID HOW
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
OPERATING SYSTEM: PC-DOS/MS-DOS

```

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,882A
FILING DATE: JUNE 23, 1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 9901/238653
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEO ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 1263 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-860-882A-56

Alignment Scores:
Pred. No.: 7,49e-62 Length: 1263
Score: 567.00 Matches: 111
Percent Similarity: 58.36% Conservative: 46
Best Local Similarity: 41.26% Mismatches: 72
Query Match: 42.38% Indels: 40
DB: 2 Gaps: 5

US-09-980-881A-4 (1-246) x US-08-860-882A-56 (1-1263)
QY 1 AlaSerAlaSerTrpTrpGluGlnTrpHisSerLeuAsnGluLeuTrpSerTrpIleGlu 20
Db 325 GCACAGAGACAGATTAAGAGATGAGATACACACAGTGGGAACGATTAAGCGTTGGACTCAA 384
QY 21 PheIleThrGluArgHisProAspMetLeuTrpLysIleHisIleGlySerSerPheGlu 40
Db 385 CAAATGCGCCACTGAGATACACAGCCCTCATCTCTCGCAGTGTATCGAACCAATTTGAG 444
QY 41 LysTrpProLeuTrpValLeuLysValSerGlyLysGluGlnThrAlaLysAlaIle 60
Db 445 GGCAGCGGCTATTACTCTCGAAGGTT---GCCAAAGTCGACAAATGAAGCTCGCAATT 501
QY 61 TrpIleAspCysGlyIleHisAlaArgIleuTrpIleSerProAlaPheCysLeuTrpPhe 80
Db 502 TTCATGACGTGGTTCATGACCCAGACAGATGATTTCTCGCATTTCTGCCAGTGGTTT 561
QY 81 Ile----- 81
Db 562 GTAAGAGAGCGTGTGACTATGAGACGTGATCCAAAGTGCAGAGACTTCTCGCAAG 621
QY 82 -----GlyHis----- 83
Db 622 TTAACTTTTATGTCCTGCTGCTGCTCAATATTGATGGCTTACATCTACACCTGACCAAG 681
QY 84 AsnArgMetTrpArgLysAsnArgSerPheTrpAlaAsnHisCysIleGlyThrAsp 103
Db 682 AGCGATTTTGGAGAAAGACTCGCTCCACCATCTAGTATCTACTGATTTGGACAGAC 741
QY 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluAlaSerSerSerCys 123
Db 742 CCCACAGAAATTTT---GATGCTGTTGGTGTGAATTTGGAGCCTCTCGAAACCCCTGT 798
QY 124 SerGluThrTrpCysGlyLeuTrpProGluSerGluProGluValLysAlaValAlaSer 143
Db 799 GATGAAGACTTACTGTGACCTGCCGACAGCTGTGAAGAAGACCAAGCCCTGGCTGAT 858
QY 144 PheLeuArgArgAsnIleAsnGlnIleLysAlaTrpIleSerMetHisSerTrpSerGln 163
Db 859 TTCATCCGCAACAACTCTCTTCATCAAGGATATCTGACATCTGACATCTGATCTCCCA 918
QY 164 HisIleValPheProTrpSerTrpThrArgSerLysSerLysAspHisGluLeuSer 183

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Db 919 ATGATGATCTACCTTACTCATATGCTTACAAACCTGGTGAGAACATGCTGAGTTGAT 978
 Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluYThrSerLysAsnThrArgTyrThr 203
 Db 979 GCCCTGGCTAAAGCTACTGTGAAAGACTT---GCCCTACCTGCACGGCAGCAGTACACA 1035
 Qy 204 HisGlyHisGlySerGluThrLeuYrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
 Db 1036 TATGGCCCGGAGGTACAAACATCATCTGCTGCTGGGGCTGTGACAGACTGGGCTTAT 1095
 Qy 224 AspleuGlyIleLysTyrSerPheThr 232
 Db 1096 GACCAAGAAATCAGATATTCCTTACC 1122

RESULT 15

US-09-011-769A-38
 Sequence 38, Application US/09011769A
 Patent No. 6436691
 GENERAL INFORMATION:

APPLICANT: SLATER, Anthony M.
 BLAKEY, David C.
 DAVIES, David H.
 HENNAM, John F.
 HENNEQUIN, Laurent F.A.
 MARSHAM, Peter R.
 DOWELL, Robert I.

TITLE OF INVENTION: Chemical Compounds
 NUMBER OF SEQUENCES: 87

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Pillsbury Madison & Sutro, LLP
 STREET: 1100 New York Ave., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A
 FILING DATE: 13-Feb-1998
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB96/01975
 FILING DATE: 13-AUG-1996
 APPLICATION NUMBER: GB 9612295.7
 FILING DATE: 12-JUN-1996
 APPLICATION NUMBER: GB 9611019.2
 FILING DATE: 25-MAY-1996
 APPLICATION NUMBER: GB 9516810.0
 FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1263 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-011-769A-38

Alignment Scores:

Pred. No.: 7,49e-62 Length: 1263
 Score: 567.00 Matches: 111
 Percent Similarity: 58.36% Conservative: 46
 Best Local Similarity: 41.26% Mismatches: 72
 Query Match: 42.38% Indels: 40
 DB: 4 Gaps: 5

US-09-980-881A-4 (1-246) x US-09-011-769A-38 (1-1263)

Qy 1 AlaSerAlaSerTyrTyrGluIntYrHisSerLeuAsnGluIleTyrSerTrpIleGlu 20
 Db 325 GCAACAGGACACAGTTATGAGAAATACAAACAGTGGGAACAGCTGAGGCTTGACTCAA 384
 Qy 21 PheIleThrGluArgHisProAspMetLeuThrLysIleHisIleGlySerSerPheGlu 40
 Db 385 CAAGTCGCCACAGAACATCCACCCCTCATCTCCAGTGTATGGAACCAATTTGAG 444
 Qy 41 LysTyrProLeuTyrValLeuLysValSerGlyLysGluIntThrAlaLysAsnAlaIle 60
 Db 445 GGACCGCGCATTTTACTCTCTGAAGCTT---GCCAAAGCTGGCAAAATTAAGCTGCATT 501
 Qy 61 TrpIleAspCysGlyIleHisAlaArgGluTrpIleSerProAlaPheCysLeuTrpPhe 80
 Db 502 TTCATGAGACTGTGTGTTTCCATGCCAGAGATGATTTCTCTGCATTTCCGACAGTGT 561
 Qy 81 Ile-----GlyHis----- 81
 Db 562 GTTAGAGAGGCTGTCTGTAACCTATGAGACGTGAGATCCAGATGACAGAGCTTCGACAAG 621
 Qy 82 -----GlyHis----- 83
 Db 622 TTAGACTTTTATGCTCTGCTGCTGCTCATATTTGATGCTTACATCTACACCTGGACCAAG 681
 Qy 84 AsnArgMetTrpArgLysAsnArgSerPheTyrAlaAsnAsnHisCysIleGlyThrAsp 103
 Db 682 ACCCGATTTTGGAGAAAGCTCGCTCCACCACTGATGATGATGATGATGATGATGATGAT 741
 Qy 104 LeuAsnArgAsnPheAlaSerLysHisTrpCysGluGluGlyAlaSerSerSerCys 123
 Db 742 CCCAACAGAAATTTT---GATGCTGTGTGTGTAATTTGAGAGCTCTCGAAACCCCTGT 798
 Qy 124 SerGluThrTyrCysGluLeuTyrProGluSerGluProGluValLysAlaValAlaSer 143
 Db 799 GATGAACTTACTGTGAGACCTGCCGAGAGCTGTGAAAGAAACCAAGCCCTGGCTGAT 858
 Qy 144 PheLeuArgArgAsnIleAsnGluIleLysAlaTyrIleSerMetHisSerTyrSerGln 163
 Db 859 TTCATCCGCAACAACTCTTCATCCAGGATATCTGACATCCATCCATCTGATCCCAA 918
 Qy 164 HisIleValPheProTyrSerTyrThrArgSerLysSerLysAspHisGluLeuSer 183
 Db 919 ATGATGATCTACCTTACTCATATGCTTACAAACCTCGAGAGAACAAATCTGAGTTGAAT 978
 Qy 184 LeuValAlaSerGluAlaValArgAlaIleGluYThrSerLysAsnThrArgTyrThr 203
 Db 979 GCCCTGGCTAAAGCTACTGTGAAAGACTT---GCCCTACCTGCACGGCAGCAGTACACA 1035
 Qy 204 HisGlyHisGlySerGluThrLeuYrLeuAlaProGlyGlyGlyAspAspTrpIleTyr 223
 Db 1036 TATGGCCCGGAGGTACAAACATCATCTGCTGCTGGGGCTGTGACAGACTGGGCTTAT 1095
 Qy 224 AspleuGlyIleLysTyrSerPheThr 232
 Db 1096 GACCAAGAAATCAGATATTCCTTACC 1122

Search completed: May 19, 2003, 06:23:15
 Job time : 33.9746 secs

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